

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/57272 A2(51) International Patent Classification⁷: **C12Q 1/68**94043 (US). **RANK, David, R.** [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00663

(22) International Filing Date: 30 January 2001 (30.01.2001)

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(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

(81) Designated States (*national*): AE, AG, AI, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).(71) Applicant (*for all designated States except US*): **MOLECULAR DYNAMICS, INC.** [—/US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).

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Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/57272 A2

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file pto_PLACENTA.txt, created 24
25 January 2001, having 26,548,337 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25 Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,
30 particularly those with polygenic etiology.

Summary of the Invention

35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
25 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,232 or a complementary sequence or a fragment thereof . 35 wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
10 placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent
5 labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third
10 or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

15 In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the
20 invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample
25 derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of
30 human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic
35 genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
15 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

20

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner
5 *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

10 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick
15 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
20 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
25 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
30 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
35 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
5 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
10 portion thereof set out in exon SEQ ID NOS.:.. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
15 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
25 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
30 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

35 As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by
10 microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the
20 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e^{-30}$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e^{-30}$ (1×10^{-30}) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

35 FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained
5 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence
10 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
15 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

20 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
25 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
30 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
35 in the present invention include GenBank, and particularly

include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR
(nonredundant) divisions. GenBank is produced by the
National Institutes of Health and is maintained by the
5 National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
eukaryotic organisms will also prove useful as genomic
10 sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
15 the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
20 mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into
25 process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
given genomic region. In such case, the input often will
30 be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
experimental confirmation is identified. Experimental
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, *e.g.*, syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query
20 can be generated that takes into account the initial
negative result.

When query 20 returns sequence meeting the query
5 criteria, the returned sequence is then passed to optional
preprocessing 24, suitable and specific for the desired
analytical approach and the particular analytical methods
thereof to be used in process 25.

Preprocessing 24 can include processes suitable
10 for many approaches and methods thereof, as well as
processes specifically suited for the intended subsequent
analysis.

Preprocessing 24 suitable for most approaches and
methods will include elimination of sequence irrelevant to,
15 or that would interfere with, the subsequent analysis.
Such sequence includes repetitive sequence, such as Alu
repeats and LINE elements, vector sequence, artificial
sequence, such as artificial polylinkers, and the like.
Such removal can readily be performed by identification and
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the
genomic sequence returned by query 20 with public or
private databases containing known repetitive sequence,
vector sequence, artificial sequence, and other artifactual
25 sequence. Such comparison can readily be done using
programs well known in the art, such as CROSS_MATCH, or by
proprietary sequence comparison programs the engineering of
which is well within the skill in the art.

Alternatively, or in addition, undesirable,
30 including artifactual, sequence can be identified
algorithmically without comparison to external databases
and thereafter removed. For example, synthetic polylinker
sequence can be identified by an algorithm that identifies
a significantly higher than average density of known
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving
10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such
15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
20 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in
25 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the
30 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression
35 of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the
10 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with
15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer
25 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify
30 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

30 Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for
5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the
10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual,
15 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,
25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes
30 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single
35 exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
35 libraries targeted at a particular biological question,

R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
5 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
15 determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
20 present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
25 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

30 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the
30 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

 This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
20 patterns.

 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

 Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their
5 complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower
10 percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual
15 probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the
20 present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear
25 genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the
30 ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present
35 invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence
5 drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which
10 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

15 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
20 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
25 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, *Reviewed in Schena et al.*, and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
30 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
35 Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83
10 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue,
15 density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be
20 indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles
25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus,
30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80
35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show
5 predictions of a plurality of different functions.
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity
5 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
10 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
15 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
25 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for
respective labeling thereof. Additional functional
information can be provided in the form of circles 86 (86a,
86b, 86c), where the diameter of the circle can be used to
indicate expression intensity. As discussed infra, such
relative expression (expression ratios) and absolute
expression (signal intensity) can be expressed using
normalized values.

Where display 80 is used as a graphical user
interface, rectangle 85 can be used as a link to further
information about the assay. For example, where the assay
is one for gene expression, each rectangle 85 can be used
to link to information about the source of the hybridized
mRNA, the identity of the control, raw or processed data
from the microarray scan, or the like.

FIG. 4 is a rendition of display 80 representing
gene prediction and gene expression for a hypothetical BAC,
showing conventions used in the Examples presented infra.
BAC sequence ("Chip seq.") 89 is presented, with the
physically assayed region thereof (corresponding to
rectangle 84 in FIG. 3) shown in white. Algorithmic gene
predictions are shown in field 81, with predictions by
GRAIL shown, predictions by GENEFINDER, and predictions by
DICTION shown. Within rectangle 87, regions of sequence
that, when used to query expression databases, return
identical or similar sequences ("EST hit") are shown as
white rectangles (corresponding to rectangles 88 in FIG.
3), gray indicates low homology, and black indicates
unknowns (where black and gray would correspond to
rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of
sequence, uninterrupted from left to right, longer
sequences are usefully represented by vertical stacking of
such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis, caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease, neurogenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, it is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of
5 expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in
10 other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which
15 are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was
20 measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten
25 tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have
30 significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon
35 microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
5 46(3):425-8 (1999)), in drug discovery screens (see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
10 Expression Profile Analysis of Human Breast Cancer
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
15 appreciated that even those probes that show no change in
expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
20 failure of the agent to change a gene's expression level is
evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
25 lead compound discovery or in subsequent screening of lead
compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

30 WO 99/58720 provides methods for quantifying the
relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);
5 Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase
35 hybridization, however – that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically
5 synthesized using commercial peptide synthesizing equipment
and well known techniques. Procedures are described, *inter
alia*, in Chan *et al.* (eds.), Fmoc Solid Phase Peptide
Synthesis: A Practical Approach (Practical Approach Series,
(Paper)), Oxford Univ. Press (March 2000) (ISBN:
10 0199637245); Jones, Amino Acid and Peptide Synthesis
(Oxford Chemistry Primers, No 7) , Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

15 It is, therefore, another aspect of the invention
to provide peptides comprising an amino acid sequence
translated from SEQ ID NOS.: 13,233 - 26,232. Such amino
acid sequences are set out in SEQ ID NOS: 26,233 - 38,837.
Any such recombinantly-expressed or synthesized peptide of
20 at least 8, and preferably at least about 15, amino acids,
can be conjugated to a carrier protein and used to generate
antibody that recognizes the peptide. Thus, it is a
further aspect of the invention to provide peptides that
have at least 8, preferably at least 15, consecutive amino
25 acids.

The following examples are offered by way of
illustration and not by way of limitation.

30 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

35 All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
15 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
35 gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not
5 span repetitive sequence was then chosen for amplification,
as were all consensus ORFs longer than 500 bp. This method
approximated one exon per gene; however, a number of genes
were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
10 fewer than 250 bp in length do not bind well to the amino-
modified glass surface of the slides used as support
substrate for construction of microarrays; therefore,
amplicons were designed in the present experiments to
approximate 500 bp in length.

15 Accordingly, after selecting the largest ORF per
gene bin, a 500 bp fragment of sequence centered on the ORF
was passed to the primer picking software, PRIMER3
(available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
20 additional sequence was commonly added to each ORF-unique
5' primer, and a second, different, additional sequence was
commonly added to each ORF-unique 3' primer, to permit
subsequent reamplification of the amplicon using a single
set of "universal" 5' and 3' primers, thus immortalizing
25 the amplicon. The addition of universal priming sequences
also facilitates sequence verification, and can be used to
add a cloning site should some ORFs be found to warrant
further study.

The ORFs were then PCR amplified from genomic
30 DNA, verified on agarose gels, and sequenced using the
universal primers to validate the identity of the amplicon
to be spotted in the microarray.

Primers were supplied by Operon Technologies
(Alameda, CA). PCR amplification was performed by standard
35 techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
15 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
30 sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays
5 prepared according to Example 1 were hybridized in a series
of simultaneous two-color fluorescence experiments to (1)
Cy3-labeled cDNA synthesized from message drawn
individually from each of brain, heart, liver, fetal liver,
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100
10 cells, and (2) Cy5-labeled cDNA prepared from message
pooled from all ten tissues and cell types, as a control in
each of the measurements. Hybridization and scanning were
carried out using standard protocols and Molecular Dynamics
equipment.

15 Briefly, mRNA samples were bought from commercial
sources (Clontech, Palo Alto, CA and Amersham Pharmacia
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were
incorporated during separate reverse transcriptions of 1 µg
of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
20 and 2 µg random 9mer primers as follows. After heating to
70°C, the RNA:primer mixture was snap cooled on ice. After
snap cooling on ice, added to the RNA to the stated final
concentration was: 1X Superscript II buffer, 0.01 M DTT,
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
30 column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_αt1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; 5 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose 10 expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 15 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 25 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 35 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue
5 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,
10 in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-
15 derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the
20 microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further
25 studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

30

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in
30 the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
35 chromosome RNA-binding motif (Chai et al., *Genomics*

49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature
 5 (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.
 10 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average
 15 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be
5 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show
10 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes.
15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very
20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following
25 colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and
30 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
5 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
10 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
25 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
30 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus
35 presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
35 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
30 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
35 been shown to be expressed - the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26696	6				
912	14087	27162	9.88				
1070	14236		3.01				
1330	14487	27556	10.9				
1645	14787	27982	1.82				
1686	14818	27901	4.94				
1764	14913	28008	1.03				
1786	14937	28030	1.67				
1794	14943	28038	8.53				
1939	15082	28183	1.57				
2034	15175	28285	2.66				
2234	15368	28487	3.39				
2383	15484	28616	2.53				
3255	15429	29447	3.75				
3637	16702	29713	1.48				
3604	16768	29783	10.5				
3651	16814		0.84				
3747	16908	29912	0.98				
4057	17213		0.94				
4314	17457	30446	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4396	17539	30520	0.87				
4457	17597		1.89				
4512	17651	30639	0.61				
4958	18088	31084	1.86				
6002	18131		0.6				
5157	18279	31244	5.14				
5168	18280	31255	1.24				
5371	18574	31442	1.76				
5371	18574	31443	1.76				
5638	18735		4.12				
5714	18907		7.26				
5760	18735		3.31				

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5856	19048	32354	4.22				
6146	25820	32668	1.61				
6174	19350	32696	1.92				
6546	19708		1.01				
6679	19638	33226	1.25				
6679	19638	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7569	20641	34117	1.18				
7569	20641	34118	1.18				
8251	21333	34851	1.44				
8682	21762	35298	1.14				
9061	22140	35684	0.76				
9061	22140	35685	0.76				
9734	22799	36373	3.82				
9968	23007	36602	0.56				
10086	23124	36725	1.51				
10229	23264	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11280	24346		1.76				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23935	37561	1.36				
11749	23935	37562	1.36				
11792	24792		2.09				
12057	25036	38746	1.56				
12623	25419		2.06				
12667	25628	31980	1.5				
6177	19353	32700	16.82	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 16, 17 and 18
8195	21277	34800	1.5	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9944	22983	36575	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9944	22983	36576	0.48	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10536	23670	37279	0.93	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gtf2h2) genes, complete cds
10636	23670	37280	0.93	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gtf2h2) genes, complete cds
2731	15849	28959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2731	15849	28960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2890	16198	28182	3.08	9.4E+00	AB043765.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8260	21372	34893	1.08	9.3E+00	AF130890.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35922	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7625	20695	34171	0.6	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXY-STEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(6)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31588	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9830	22685		1	9.0E+00	P09241	SWISSPROT	RI-ODOPSIN
6160	16336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3894592 3'
6510	19875	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster OpTbx3 premature mRNA, partial cds
6510	19875	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster OpTbx3 premature mRNA, partial cds
453	13649	26685	1.79	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9854	21097	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (sec2a)
11443	24504		1.98	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21426		0.98	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7501	20576		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8556	21637	35174	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8556	21637	35175	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8953	22032	35573	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35574	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33760	1.07	7.2E+00	BE179080.1	EST_HUMAN	RCO-H10613-200300-031-a07 HT0613 Homo sapiens cDNA
7299	20381	33838	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7299	20381	33839	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6798	22838		9.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11668	24746	38437	2.44	7.1E+00	P05950	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10187	23224	36818	2.76	7.0E+00	P46810	SWISSPROT	ARGININE KINASE (AK)
11528	24584	38261	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8478	21559	35093	3.17	6.9E+00	P35979	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10559	23594	37200	1.12	6.8E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10579	23614	37219	0.6	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
6092	21174	34888	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34889	1.84	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Scars melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:291860 5'
5333	22409		1.62	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 167.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5398	18600		0.86	6.6E+00	Q89028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6675	19834	33223	0.86	6.6E+00	BF672121.1	EST_HUMAN	602152573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4263427 5'
9234	20228		0.55	6.6E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.6E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37496	0.47	6.6E+00	H28330.1	EST_HUMAN	ym60f06.s1 Scars Infant brain T1NB Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10512	23547	37158	0.52	6.5E+00	BE866001.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3963989 5'
9843	22982	36574	1.34	6.2E+00	A7010901.1	NT	Schizosaccharomyces commune unknown mRNA
10787	23820	37444	0.7	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7181	20313	33758	1.6	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36855	0.49	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1168000 nt, position (6/7)
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19809	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11933	24919		3.02	5.9E+00	BE988630.1	EST_HUMAN	601645279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'
3613	16777		1.15	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20394	33855	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20303		1.34	5.6E+00	P75030	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11289	24355	37986	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37997	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11765	23951	37581	2.52	5.6E+00	Q55279	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32906	0.74	5.9E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRC4
8982	23021		0.56	5.5E+00	P13993	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24097		1.46	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.5E+00	P11690	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559	33537	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8054	21137		1.82	5.4E+00	Q91062	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANGREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8996	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELIN LV-1N; LIPOVITELIN LV-1C;
8999	22078	35619	0.93	5.4E+00	P40379	SWISSPROT	LIPOVITELIN LV-2]
10242	23277	36870	1.45	5.4E+00	Q17094	SWISSPROT	REPT PROTEIN
10242	23277	36871	1.45	5.4E+00	Q17094	SWISSPROT	REPT PROTEIN
4806	18036	31024	1.47	5.3E+00	L43126.1	NT	RHODOPSIN
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	RHODOPSIN
8270	21352		3.39	5.3E+00	P54098	SWISSPROT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
9184	22262		0.72	5.3E+00	AB034980.1	NT	HOMEOBOX PROTEIN CEH-20
11928	24914	36616	1.51	5.3E+00	Q27905	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
5590	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
10583	23618		0.96	5.2E+00	AF248070.1	NT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
11470	24529		1.93	6.2E+00	Q10136	SWISSPROT	QV4-HT0891-270400-186409 HT0891 Homo sapiens cDNA
9182	22240	35784	0.94	5.1E+00	O16005	SWISSPROT	Drosophila orientacea R1B, retrotransposable element reverse transcriptase gene, partial cds
10030	23068	36657	1.33	5.1E+00	P08182	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
6415	19584	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	RHODOPSIN
10397	23432		0.7	5.0E+00	BF308561.1	EST_HUMAN	COLICIN N IMMUNITY PROTEIN (MICROGICIN N IMMUNITY PROTEIN)
							601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
							601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10645	23679	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24624	38304	7.24	5.0E+00	Z83850.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10437	23472		0.78	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRef gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		12.39	4.8E+00	AF185255.1	NT	Embla australis histone H3 (H3) gene, partial cds
8348	21429	34953	0.6	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8738	21817		4.92	4.8E+00	AW750087.1	EST_HUMAN	PV0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240562.1	EST_HUMAN	601875654F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089716 5'
301	13517	28550	1.85	4.7E+00	BF240562.1	EST_HUMAN	601875654F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089716 5'
3347	16520	29534	1.02	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7862	21012	34522	0.59	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9397	22471	38036	1.1	4.6E+00	BE846437.1	EST_HUMAN	788g10.X1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element
9397	22471	38037	1.1	4.6E+00	BE846437.1	EST_HUMAN	788g10.X1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element
10600	23835		0.63	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
7947	20997		0.7	4.5E+00	AF126177.1	NT	Issatchenkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11804	24892	38593	1.87	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12058	25039	38747	1.53	4.5E+00	BF688941.1	EST_HUMAN	602123238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280216 5'
3105	16281	29296	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4215284 5'
3105	16281	29297	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4215284 5'
6331	19502		1.58	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (Ia) associated invariant chain
8245	19419		0.77	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7596	20696	34142	2.53	4.3E+00	Y13402.1	NT	Plasmodium falciparum R23R+var1 gene, exon 1
7792	20848	34341	0.68	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11101	24174	37809	14.74	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5634	18923		4.1	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5711	18904	32199	1.07	4.2E+00	P51826	SWISSPROT	LA-F4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5880	19070		0.71	4.2E+00	O27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
8911	20226	33657	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6811	20228	33658	1.67	4.2E+00	P13883	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8160	22238	35783	5.3	4.2E+00	AI809013.1	EST_HUMAN	W67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692.3
10122	23180	36759	1.03	4.2E+00	P31388	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10352	23387		0.47	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
7281	20344	33786	0.98	4.1E+00	BE253688.1	EST_HUMAN	60110727F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351534.5
7839	20894	34396	7.66	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7860	21010		0.64	4.1E+00	AB041523.1	NT	Pathopecien yessoensis mRNA for calcineurin A, complete cds
7863	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7863	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNL2 locus
9740	22805	36381	0.61	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22913	36498	2.25	4.1E+00	BF692425.1	EST_HUMAN	R02247938F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333209.5
10370	23105		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
10514	23549		0.52	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
11124	24196		2.15	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HMLF1
11214	24283		12.25	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051.5
3635	16789		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5675	20130	33548	0.93	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5575	20130	33547	0.93	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33546	0.89	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33547	0.89	4.0E+00	O62853	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22153	35897	0.49	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (NNOS)
10388	23403	37014	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23489	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23489	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11782	23948	37577	1.59	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.98	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
12133	25113	38817	1.34	4.0E+00	P35811	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3591	16755	28770	5	3.9E+00	X64518.1	NT	N. fabacum chitinase gene 50 for class I chitinase C
4441	17581		0.87	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 98 (MSVSP98) gene, promoter region
5775	18967	32270	2.92	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5775	18967	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6772	19627	33322	0.93	3.9E+00	AF298209.1	NT	Dicotyledonous discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19882	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
7519	20592	34086	4.25	3.9E+00	M23907.1	NT	Human MHG class II lymphocyte antigen (DPW4-beta-1) gene, exon 2
8512	21593	35128	2.44	3.9E+00	X65665.1	NT	X. laevis mRNA for M4 muscarinic receptor
11874	23902	37524	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2893	19813		1.53	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99, section 123 of the complete genome
6520	19695	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8627	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9999	23037		0.6	3.8E+00	AJ300961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
12120	25100		11.65	3.8E+00	9831294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4129	17282	30277	12.78	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8378	22454	35017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38450	2.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC.56 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC.56 Homo sapiens cDNA clone IMAGE:4277748 5'
12260	25198		1.87	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
609	13795	20814	3.76	3.6E+00	AV781055.1	EST_HUMAN	AV781055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5369	18572	31440	0.78	3.6E+00	BF316310.1	EST_HUMAN	601901868F1 NIH_MGC.19 Homo sapiens cDNA clone IMAGE:4131016 5'
8749	21828	35364	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone t508
8749	21828	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone t508
8847	21823	35464	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8847	21926	35485	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9884	22804	36488	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9884	22804	36488	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24167						
3319	19492	29509	3.21	3.6E+00	M86785.1	NT	Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds; and the translation start site has been verified (gpe), the translation start site has been verified (gpe), and repressor protein (gpr) genes, complete cds
8123	18302		1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
8341	19511	32868	0.93	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
8681	21781		0.56	3.5E+00	R19745.1	EST_HUMAN	X94008.1 Soares Infant brain INIB Homd sapiens cDNA clone IMAGE:34940 5'
9232	22310	35851	0.99	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element ;
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element contains element MSR1 repetitive element ;
9894	22743	36313	0.58	3.5E+00	AF133723.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
10739	23772	37383	0.58	3.5E+00	AF133723.1	NT	Boa taurus mRNA for Ran-binding protein 2, partial
1542	14694	27773	3.81	3.4E+00	AF284577.1	NT	Brassica napus RPB5d mRNA, complete cds
2644	15767	28882	1.07	3.4E+00	AF163278.2	NT	Homo sapiens chromosome 21, segment HS21C078
7518	20581	34065	2.33	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7880	20932	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955		0.77	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
9274	22350	35801	0.77	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9312	22388	35939	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10471	23808	37118	3.35	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11822	24811	38908	2.06	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6183	19369	32719	0.97	3.3E+00	Q08689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6183	19369	32720	0.97	3.3E+00	Q08689	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8077	21169	34678	1.03	3.3E+00	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds; and unknown genes
10681	23715	37321	1.04	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10681	23715	37322	1.04	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
513	13707	26735	1.79	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene

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4136	13707	26735	0.78	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4860	17953	30971	0.95	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (GEACAM1), mRNA
5686	18880	32170	1.18	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5686	18880	32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19603	32866	1.91	3.2E+00	P18931	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19603	32867	1.91	3.2E+00	P18931	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.86	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7852	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7852	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22308	36369	5.26	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENYLASE SMALL CHAIN)
9730	22795	36369	1.31	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10345	23380	36981	2.06	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for guanylyl cyclase C, complete cds
12219	26188	32503	2.95	3.2E+00	L38336.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5996	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHELICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7547	20819	34095	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (GTPT)
7804	20956	34095	1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8279	21361	34880	0.51	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DII) (8DI)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DII) (8DI)
9469	22575	36162	3.7	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9526	22591	36162	0.55	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10100	23138	36739	0.76	3.1E+00	7624789	NT	Chlorella vulgaris chloroplast, complete genome
10183	23230	36739	0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHELICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10543	23578	37187	4.09	3.1E+00	P46955	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11751	23937		2.45	3.1E+00	P33516	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN), MATRIX PROTEIN (ENVELOPE PROTEIN M), MAJOR ENVELOPE PROTEIN E, NONSTRUCTURAL PROTEINS NS1, NS2, NS3, NS4 AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
11771	24763		2.49	3.1E+00	S66660.1	NT	retinole acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PC07-MZ1, mRNA, 2971 nt]
13019	25670		1.17	3.1E+00	U77666.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2899	16078	28095	0.95	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18654	31633	1.29	3.0E+00	X53096.1	NT	S. aureus genes encoding Saus61 DNA methyltransferase and Saus61 restriction endonuclease
6686	19844	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6686	19844	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20398		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7346	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.62	3.0E+00	X67838.1	NT	B. napus DNA for myrosinase
10501	23538	37146	0.56	3.0E+00	Q59605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11269	24328	37067	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2F) (GC-F)
11259	24328	37968	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2F) (GC-F)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
2087	15208	28324	2.69	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AF39, section 53 of 94 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z38879.1	NT	F. pringlei gdaPA gene for P-protein of the glycine cleavage system
7380	20439	33889	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7380	20439	33900	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684	34180	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	21135	34655	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8052	21135	34656	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8288	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3
9438	22512		0.82	2.9E+00	AI002153.2	NT	602017413F1 NC1 CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4753059 5'
1486	14639	27722	4.77	2.8E+00	AF186398.1	NT	Sagittaria oedipus gene for seminal vesicle secreted protein semenogelin 1
1662	14814		3.14	2.8E+00	AL161562.2	NT	Buxus harlandii mature K (matK) gene, partial cds; chloroplast gene for chloroplast product
7480	20535	34010	5.05	2.8E+00	B393724	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
9813	22853		0.6	2.8E+00	BE565182.1	EST_HUMAN	Mus musculus endomucin (LOC53423), mRNA
10928	20535	34010	1.53	2.8E+00	B393724	NT	601342759F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
240	13462	26400	13.96	2.7E+00	6679306	NT	Mus musculus endomucin (LOC53423), mRNA
240	13462	26491	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phor3), mRNA

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Single Exon Probes Expressed in Placenta

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5869	18863	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U16047.1	NT	Ipomoea purpurea chalcone synthase (CHS), gene including complete 5'UTR and complete cds
9188	22246		2.16	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9632	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xc88ef12.x1 NCI_COAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374.3' similar to gb:M17733
10718	23751		1.94	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4796	17931	30917	5.51	2.6E+00	AF068749.1	NT	CanO-BT0281-031189-037-h04 BT0281 Homo sapiens cDNA
5665	18859	32143	2.04	2.6E+00	675560.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5665	18859	32144	2.04	2.6E+00	675560.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5947	19133		2.56	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7727	26220		1.16	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7879	20931		11.26	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27 and complete cds
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9858	22898	36481	2.86	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10563	23598		1.91	2.6E+00	6055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11281	24347	37984	2.2	2.6E+00	AF143875.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12917	26064		3.3	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1492	14645	27726	3.03	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14645	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5934	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5934	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5934	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5934	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5934	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	20020	33428	0.77	2.5E+00	D30052.1	NT	Vibrio cholerae ctaA gene and ctaB gene for cholera toxins, complete cds
7936	20968	34494	1.19	2.5E+00	AW049158.1	EST_HUMAN	QV4-FT0005-110500-205-p07 FT0005 Homo sapiens cDNA
7985	21034	34547	0.62	2.5E+00		NT	Homo sapiens elafirin, heavy polypeptide-like 1 (GLTCL1) mRNA
8304	22380	35631	1.55	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23095	36697	0.71	2.5E+00	BE297758.1	EST_HUMAN	80117679F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3631090 5'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAAJ PROTEIN
12216	25167		1.86	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3078	16254	29276	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5027	18156	31134	4.93	2.4E+00	4503362	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	16313	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20811	34085	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20811	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8408	21487		2.8	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8832	21931		1.72	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-005 PT0004 Homo sapiens cDNA
9028	22107	35648	8.99	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36954	2.31	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P08099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10528	23563	37169	1.64	2.4E+00	BE326702.1	EST_HUMAN	h63068.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.64	2.4E+00	BE326702.1	EST_HUMAN	h63068.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN N1RQ
11335	24398	38047	1.38	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKO operon and downstream
11640	24720	38413	2.44	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	14438	27507	9.98	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4237	17983		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5987	19143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7612	20882	34168	2.76	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Cat+ transporting, ubiquitous (Atp2a3), mRNA
7771	28221		2.37	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7958	21008	34518	1.28	2.3E+00	X60285.1	NT	M.mazaei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9310	22386	35938	0.62	2.3E+00	5835317	NT	Polyporus ornithinis mitochondrion, complete genome
9371	22446	36008	1.86	2.3E+00	Q11127	SWISSPROT	ALPHA-(1-3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
11041	24120	37763	2.72	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	2.3E+00	BF641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12075	25056	38764	2.14	2.3E+00	BF641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12445	25315	32091	7.41	2.3E+00	BE865237.1	EST_HUMAN	601433073F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4128	17280	30276	1.06	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4432	17572	30554	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18658	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5975	19160	32479	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6187	19363	32711	9.39	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6484	19651	33013	2.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18824		3.4	2.2E+00	AA594574.1	EST_HUMAN	IN9580231 NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	2187104.1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	z005g10.t1 Soares_t01 Homo sapiens cDNA clone IMAGE:785634 5'
7866	20920	34427	0.66	2.2E+00	P54918	SWISSPROT	ALANINE RACENASE
8294	21378	34896	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8294	21378	34897	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45838 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9542	22607		12.49	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948861 5'
9768	26860		2.12	2.2E+00	Q04708	SWISSPROT	TRANSPONSON TY1 PROTEIN A
10259	23294	36890	1.12	2.2E+00	A1290373.1	EST_HUMAN	q169b03.x1 Soares_placenta_8169weeks_2NBHP869W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36891	1.12	2.2E+00	A1290373.1	EST_HUMAN	q169b03.x1 Soares_placenta_8169weeks_2NBHP869W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF248782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076391 5'
10673	23707	37315	2.6	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR74 homolog mRNA, complete cds
11726	23912	37536	3.3	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	16016	26795	13.2	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449386.1	EST_HUMAN	U1H-B13-aid-e-08-O-J1.1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

Single Exon Probes Expressed in Placenta

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6260	19434		0.97	2.1E+00	P76357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20260	33698	3.51	2.1E+00	O70159	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dyferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20956	33466	5.88	2.1E+00	N2575.1	EST_HUMAN	Y08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:U55654
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RV2000671 5'
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1366	14520	27595	1.37	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1606	14759		3.09	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Nax-K-A1Pase beta 1 subunit mRNA, complete cds
2216	16360	28480	7.2	2.0E+00	Z76279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	16350	28481	7.2	2.0E+00	Z76279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4216	17365	30353	1.71	2.0E+00	AW694486.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I
4216	17365	30354	1.71	2.0E+00	AW694486.1	EST_HUMAN	h113c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
7722	20786		0.96	2.0E+00	P07568	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34915	4	2.0E+00	AB008676.1	NT	h113c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
8214	21296	34916	4	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34917	4	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12815	26022	31670	6.76	2.0E+00	5834843	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32202	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5715	18908	32203	4.28	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6225	19400	32750	1.2	1.9E+00	BE969695.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117808
6792	19947		0.92	1.9E+00	AW845689.1	EST_HUMAN	Gallus gallus mitochondrion, complete genome
6866	20940		1.91	1.9E+00	Q63627	SWISSPROT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
8653	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	Mus musculus inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
8653	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3849881 5'
8659	21638		3.32	1.9E+00	BF360206.1	EST_HUMAN	MRO-CT0063-071089-002-g02 CT0063 Homo sapiens cDNA
9095	22174		1.86	1.9E+00	O61781	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
							CM3-MT0114-010900-323-H12-MT0114 Homo sapiens cDNA
							ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.8E+00	AA660125.1	EST_HUMAN	ab94404.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10790	23823	37447	0.67	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3162	16337	29346	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	29370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. POC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	29371	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. POC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32758	2.02	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19692		1.28	1.8E+00	BF683327.1	EST_HUMAN	602136470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6879	20031	33441	1.19	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069	33479	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE- (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.68	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8308	21390	34914	0.68	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9056	22134	35679	2.28	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.78	1.8E+00	R31042.1	EST_HUMAN	yh72e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9462	22519	36081	0.82	1.8E+00	AW860004.1	EST_HUMAN	QV0-O10030-070300-148-a03 O10030 Homo sapiens cDNA
9886	23034	36626	0.47	1.8E+00	P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36894	0.94	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10460	23526		4.71	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12687	25444		6.01	1.8E+00	9503404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
13005	25887	31854	1.45	1.8E+00	BF212412.1	EST_HUMAN	60181374F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1132	14297	27352	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345	15476	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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2446	16573	28702	1.49	1.7E+00	AI141067.1	EST_HUMAN	α43H05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4881	17718	30701	0.98	1.7E+00	Q80114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32216	1.73	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171298-127-c05 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171298-127-c05 BT0282 Homo sapiens cDNA
6141	18319	32661	3.02	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6682	19840	33230	0.67	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDP)]
7367	20446	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHELICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7367	20446	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHELICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6755713	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall), mRNA
8252	21334	34852	0.61	1.7E+00	BF530630.1	EST_HUMAN	802071917F1 NCL CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4214669 5'
8739	21818	35352	0.76	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8828	21907	35519	1.63	1.7E+00	BF306000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8801	21980	35520	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8801	21980	35520	0.66	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35833	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	25858	35981	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9350	25858	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9808	22846		1	1.7E+00	AF161380.1	NT	Homo sapiens HSPC262 mRNA, partial cds
10375	23410		0.54	1.7E+00	AW953681.1	EST_HUMAN	EST365751 IMAGE:365751 MAGC Homo sapiens cDNA
10857	23890	37509	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
10857	23890	37510	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
11896	24694	38582	1.67	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12523	25356	32066	1.94	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11 MSR1 repetitive element;
2090	15230	28352	19.53	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2101	15241	28362	4.14	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2107	16246	28367	1.26	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2357	16488		0.97	1.6E+00	X86373.1	NT	B. napus gene encoding endo-polygalacturonase
3026	16202	28225	1.22	1.6E+00	W56426.1	EST_HUMAN	zid2501.1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D28806 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3857	17017		1.08	1.6E+00	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17204		6.05	1.6E+00	BF570077.1	EST_HUMAN	802186035T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17612	30590	1.25	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17612	30591	1.25	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.6E+00	AF127897.1	NT	Salmonella typhimurium diffractin receptor (SDF2) gene, partial cds
5194	18316	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6Galinacil gene, exon 2
5194	18316	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6Galinacil gene, exon 2
5948	19134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	19218	32540	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6589	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060900-145-502 UT0073 Homo sapiens cDNA
6549	20002	33411	1.05	1.6E+00	AW294881.1	EST_HUMAN	U1H-B12-alt-B-04-Q-U1.s1 NCL OGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33938	2.37	1.6E+00	BE597267.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MYIN HOMOLOG
8574	21655	35196	3.3	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35898	0.49	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9559	25857	34615	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9559	25857	34616	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermotoga maritima elhancidicus D-xylose-binding protein (xyf) gene, complete cds
9935	22974	36596	1.49	1.6E+00	T41290.1	EST_HUMAN	ph656_19/TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph656_19/1 TV
10388	23423	37029	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-L10016-090200-100-d07 L10016 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-L10016-090200-100-d07 L10016 Homo sapiens cDNA
10552	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24099	37728	1.77	1.6E+00	P64817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11082	19218	32540	4.8	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
12006	24691	38695	3.68	1.6E+00	AF104313.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
33	13271	26275	2.95	1.6E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AF39, section 32 of 94 of the complete genome
636	13821		1.81	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagidin) (Adam15), mRNA
2481	15608	28732	1.56	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2584	15709	28828	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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3208	16608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3482	16628	29649	0.77	1.5E+00	AE001945.1	NT	Delinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5848	19036	32342	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12710.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.;
5848	19036	32343	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12710.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.;
6538	19088	33072	2.43	1.5E+00	RI17879.1	EST_HUMAN	yg10a02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 5'
7278	20361		1.68	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33853	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stratiococcus schizobrain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8313	21393	34920	0.9	1.5E+00	BE887446.1	EST_HUMAN	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8846	21925	35463	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9218	22296		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35963	0.51	1.5E+00	BF217818.1	EST_HUMAN	601882862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9884	22733	36303	0.85	1.5E+00	R81928.1	EST_HUMAN	y03h01.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36459	1.6	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261089-008-009 CT0192 Homo sapiens cDNA
10064	23102	36705	6.49	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10258	23293		1.85	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	ze38g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361308 5'
11684	24683	36373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		7.68	1.5E+00	X07380.1	NT	Malze mitochondrial RNA-Ser gene and rRNA-Phi pseudogene
11929	24915	38617	1.39	1.5E+00	AI400768.1	EST_HUMAN	tg94d08.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11929	24915	38618	1.39	1.5E+00	AI400768.1	EST_HUMAN	tg94d08.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12616	26095	31662	1.61	1.5E+00	D63490.1	NT	Human mRNA for KIAA0146 gene, partial cds
12765	26508		3.92	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12888	26589		2.17	1.5E+00	5978492	NT	Rattus norvegicus 5'-Lipoxigenase (ALOX5), mRNA
13220	26794	31888	1.31	1.5E+00	BF223935.1	EST_HUMAN	7682003.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13268	26271	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP568M0122 protein (DKFZP568M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP568M0122 protein (DKFZP568M0122), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2411	15541		9.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15851	28984	1.7	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16583		0.79	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30493	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-288-H08 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-288-H08 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF681547.1	EST_HUMAN	90215887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18887	31705	1.73	1.4E+00	AW054876.1	EST_HUMAN	W45907.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5645	18839		6.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32839	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	26214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6981	20189	33814	0.8	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0008-300300-132-B12 NN0008 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7464	20531	34005	1.14	1.4E+00	AW487780.1	EST_HUMAN	he2305.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7514	20588	34062	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7514	20588	34063	0.7	1.4E+00	P55258	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8530	21611		0.72	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8894	22073		5.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9295	22371	35920	1.65	1.4E+00	R20459.1	EST_HUMAN	YG33112.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9308	22472	36038	3.83	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-307269-012-05 B.T0313 Homo sapiens cDNA
9432	22506	36072	0.65	1.4E+00	AF134944.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF575545.1	EST_HUMAN	902133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-281098-008-C04 HT0198 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-281098-008-C04 HT0198 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23885	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11488	24557	38232	4.52	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11691	24689	38379	3.46	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24689	38380	3.48	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. reiti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. reiti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.99	1.4E+00	11545838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
684	13776		1.66	1.3E+00	Z73640.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-trisporate dehydrogenase
925	14100	27164	2.79	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
1326	14482	27649	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27950	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14542		0.98	1.3E+00	U01730.2	NT	Cdx lacryme-jobi dihydrodipicolinate synthase (dapa) gene, complete cds
1641	14783		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPB genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2815	15739		1.81	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
3005	16180	29201	0.86	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Sptn1), mRNA
3686	16848	29857	1.14	1.3E+00	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5631	18826	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M33496.1	NT	D. melanogaster no-on-transient A gene product, complete cds
6890	20042		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P48940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7092	20198	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7249	20332	33779	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7616	20696	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21576	35112	1.78	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
8642	21722	35259	2.28	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8758	21837	35378	1.05	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21886		1.87	1.3E+00	6910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22069	35609	0.89	1.3E+00	AJ927629.1	EST_HUMAN	wc86a07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35976	0.61	1.3E+00	H42981.1	EST_HUMAN	y086c03.s1 Soares breast 3NH-Bst Homo sapiens cDNA clone IMAGE:183076 3'
9347	22423	35977	0.51	1.3E+00	H42981.1	EST_HUMAN	y086c03.s1 Soares breast 3NH-Bst Homo sapiens cDNA clone IMAGE:183076 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylaseN-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S. salba pht-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S. salba pht-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	w03f03.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2528477 3' similar to gb:M31522
9871	22911	36496	1.85	1.3E+00	Q00754	SWISSPROT	TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9952	23091	36584	1.21	1.3E+00	AJ927629.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
10031	23069	36688	0.88	1.3E+00	AJ223962.1	NT	wc85807.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23069	36689	0.88	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10070	23109	36711	3.93	1.3E+00	BE963379.2	EST_HUMAN	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10130	23168		0.57	1.3E+00	AI559944.1	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
10353	23388	36906	0.5	1.3E+00	AF061251.1	NT	lq77a12.x1 NCI CGAP_U01 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723
10353	23388	36907	0.5	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10418	23453	37059	1.88	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10435	23470	37076	1.39	1.3E+00	M29953.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10811	23844		0.99	1.3E+00	AL163302.2	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10838	23871	37493	0.47	1.3E+00	AI990946.1	EST_HUMAN	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10851	23884		0.53	1.3E+00	8923637	NT	Homo sapiens chromosome 21 segment HS21C102
							wc32e10.x1 NCI CGAP_G03 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
							Q19881 THIOREDOXIN REDUCTASE ;
							Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7949160	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo86c03.at Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo86c03.at Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10862	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	xp09603.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11923	24909	38610	2.28	1.3E+00	Z98882.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
11984	24978		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketocacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	AF187873.1	NT	Carica papaya inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	802023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	25898		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	AF187035.1	NT	Sturmira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
13231	25981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
667	13853	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	z22208.at Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
846	14024	27082	1.52	1.2E+00	P03228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
846	14024	27083	1.52	1.2E+00	P03228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
846	14024	27084	1.52	1.2E+00	P03228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
901	14076		1.21	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PR03077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Elleis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2066	15207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	29359	1.06	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	29421	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.67	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	29625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16964	29867	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-q06_1 FT0175 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16805	29625	1.06	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4594	17731		1.97	1.2E+00	M87050.1	NT	Rattus rattus cardiac AEC3 gene, exons 1-23
4645	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30808	2.03	1.2E+00	AF150495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T. pinnaeum chloroplast (bcl. gene, partial
5554	18751	31788	1.13	1.2E+00	U20780.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18868	32162	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0161-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19108		0.66	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5965	19180	32502	0.77	1.2E+00	X74885.1	NT	Homo sapiens zinc finger protein ZNF161 (ZNF161) gene, complete cds
6280	19454	32802	2.45	1.2E+00	X74885.1	NT	D.hydrel ay1 repeat cluster DNA, fragment D
6342	19512	32869	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19589	32953	1.28	1.2E+00	X86084.1	NT	C-glutamicum pla gene and ackA gene
6420	19589	32954	1.29	1.2E+00	X89084.1	NT	C-glutamicum pla gene and ackA gene
6463	19630	32991	36.06	1.2E+00	AA759254.1	EST_HUMAN	af84g12.s1 Soares_basile_NH-T Homo sapiens cDNA clone 1322374.3'
							y39b12.s1 Soares melanocyte 2Nbr-M Homo sapiens cDNA clone IMAGE:273599 3' similar to
6566	19728	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	gjm87935jHUMAAU472 Human carcinoma cell-derived Alu RNA transcript. (RNA); gb:J04970
6630	19760	33178	0.62	1.2E+00	P17671	SWISSPROT	CARBOXYPEPTIDASE M PRECURSOR E75-A
6634	19763	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	ECODYSONE-INDUCIBLE PROTEIN E75-A
7055	20108	33524	1.72	1.2E+00	AB029010.1	NT	MR3-ST0161-140200-013-c05 ST0191 Homo sapiens cDNA
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
							Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	zq38f05.r1 Stratagene RNT neuron (8937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to
7403	20481		0.71	1.2E+00	AJ271735.1	NT	gb:U10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7542	25847	34092	1.85	1.2E+00	AV734595.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
7828	20883	34385	2.81	1.2E+00	X74207.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7997	21047	34580	0.6	1.2E+00	BE787448.1	EST_HUMAN	AV734595 cda Homo sapiens cDNA clone cdAAAFH03 5'
8767	21846	35387	3.19	1.2E+00	AB030303.1	NT	Lactis pyrD and pyF genes
							601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT
							(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
8863	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	GLUCOSYL TRANSFERASE
9077	22156		0.7	1.2E+00	7708271	NT	Homo sapiens CGI-30 protein (LOC31611). mRNA
9226	22304	35847	1.81	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9440	22514	36078	0.51	1.2E+00	H48596.1	EST_HUMAN	yq80a06.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9598	22653	36224	3.79	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HUMHMO1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo1a01
10135	23173	36771	3.6	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10332	23587		0.82	1.2E+00	AB009669.1	NT	Homo sapiens kidney gene, exon 1
11432	24493	38158	1.69	1.2E+00	M38686.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PINO-ST0264-16199-001-d01 ST0264 Homo sapiens cDNA
11668	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37556	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Maize mitochondrial F.O.A1Pase protolipid (subunit 8) gene
12471	25994	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001516.1	NT	Bacillus halodurans genomic DNA, section 9/14
13218	25793		2.66	1.2E+00	AA077909.1	EST_HUMAN	7H11A06 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	28703	1.11	1.1E+00	D86680.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW595383.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-ek-f-02-Q-J1.e1 NIH_MGC 52 Homo sapiens cDNA clone IMAGE:3074834 3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29595	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	16740	29757	1.02	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3870	16833	29844		1.1E+00	AI808380.1	EST_HUMAN	wf54h1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359481 3' similar to
3812	16972	29974	1.16	1.1E+00	AE003898.1	NT	SW_F531_HUMAN Q12868 P53-BINDING PROTEIN 53BP1
3812	16972	29975	1.16	1.1E+00	AE003898.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
4054	17210	30220	1.03	1.1E+00	8922641	NT	H. parahemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4130	17283	30278	0.72	1.1E+00	6755205	NT	Homo sapiens probasome (prosome, macropair) subunit, beta type 7 (Pamb7), mRNA
4331	17474		0.82	1.1E+00	5835331	NT	R. uniconis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18486.1	NT	African swine fever virus, complete genome
5180	18302	31265	2.06	1.1E+00	X78425.1	NT	E. faecalis pbb5 gene
5422	18623	31599	1.49	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18824	32218	14.33	1.1E+00	BE60184.1	EST_HUMAN	60162770R1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3825835 3'
5760	18942	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	q885c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6404	19573	32835	0.59	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	1.1E+00	R06037.1	EST_HUMAN	ye89603.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124924 5'
8958	20009	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7447	20524	33997	0.58	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.87	1.1E+00	BF683714.1	EST_HUMAN	802139978F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20726	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20726	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.35	1.1E+00	AL161988.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11987980	NT	Mus musculus silent melting type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8326	21407	34934	3.2	1.1E+00	BF603996.1	EST_HUMAN	802082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8416	21497	35029	0.91	1.1E+00	AJ478339.1	EST_HUMAN	hm39h11.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2160549 3'
8835	22014	35554	0.86	1.1E+00	AB003098.1	NT	Acetabularia calciculus mitochondrial COXI-like gene
9015	22094	35634	0.87	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9126	22203	35748	0.53	1.1E+00	AJ079946.1	EST_HUMAN	023405.x1 Soares_NHMP1_ST Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080	36348	0.75	1.1E+00	BE384876.1	EST_HUMAN	801276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9828	22868	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9853	22923		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9874	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaeF, psaeF, adhesin (psaeA), chaperone (psaeB), and usher (psaeC) genes, complete cds
10038	23076	36876	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
10141	23179	36777	4.09	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23864	37486	0.56	1.1E+00	AJ878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618282 5' similar to gb:D10522
10856	23970	37600	1.97	1.1E+00	11087364	NT	Human mRNA for 80K-L protein, complete cds, (HUMAN);
10947	24029		3.14	1.1E+00	AF068942.1	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
11343	24405	38055	3.72	1.1E+00	L16877.1	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
11361	18486		2.74	1.1E+00	8822973	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
							Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11368	24427	38083	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11369	24427	38084	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38409	3.99	1.1E+00	AB09699.1	EST_HUMAN	wf76e11.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381548 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312	32070	1.82	1.1E+00	P07886	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	25371	32070	3.56	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein T676 mRNA, partial cds
12689	25980		1.86	1.1E+00	AF234169.1	NT	Dictyostellum discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116	13347	26374	2.1	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021694.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13781	26800	1.44	1.0E+00	AJ251680.1	NT	Girardinia litorea mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13879		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1795	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	16679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	16679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element :
2940	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2940	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.95	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME I
3289	16443	29463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element :
3459	16628		0.73	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.61	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4180	17330	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17533		0.72	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31568	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
8248	19422	32768	1.67	1.0E+00	AW452782.1	EST_HUMAN	UI-H-B18-alk-d-09-0-UI-1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068980 3'
8618	19778	33167	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
8671	19830	33219	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
8787	19923		1.07	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
8795	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938382 5'
8795	19950	33350	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938382 5'
8916	20231	33694	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding vdxoxopsin
7288	20371	33828	1.15	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 (cattle, pulmonary artery endothelial cells, mRNA, 2028 nt)
7647	20715		9.68	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF102531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34492	6.02	1.0E+00	AA775191.1	EST_HUMAN	ac79508.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:888791 3'
8019	21070		0.72	1.0E+00	BF679213.1	EST_HUMAN	602153792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8148	21230	34749	1.65	1.0E+00	BE868297.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8148	21230	34750	1.65	1.0E+00	BE868297.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8335	18495		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21626	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	21762		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLSTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.54	1.0E+00	Q9Y6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLSTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21788	35322	0.54	1.0E+00	Q9Y6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLSTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	25858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-H10229-181089-011-908 HT0229 Homo sapiens cDNA
8776	21855	35387	1.15	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8822	22001	35640	1.8	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9471	22528	36091	1.95	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9882	22731	36301	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9882	22731	36302	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9810	22850	36428	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9816	22856	36435	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10318	23353	36981	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10318	23353	36982	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10408	23443	37050	0.69	1.0E+00	A077920.1	EST_HUMAN	0y1507.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1655901 3'
10633	23668	37175	3.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
10884	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10884	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10728	23781	37398	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	S90825.1	NT	PBR1 proline-rich protein (ntion 3) [human, Genomic, 898 nt]
11342	24405	38064	1.46	1.0E+00	AA701494.1	EST_HUMAN	zh63b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11825	24814		1.62	1.0E+00	L47813.1	NT	Picea glauca EMB13 mRNA
12329	25238		5.48	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12876	25451		2.67	1.0E+00	AW876184.1	EST_HUMAN	EST388283 MAOE reassurances, MAGN Homo sapiens cDNA
3693	18855		1.04	9.9E-01	AF174385.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
6752	18944	32246	8.8	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5990	19175	32496	0.83	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9481	22518		1.68	9.9E-01	U65687.1	NT	Lycopodium esculentum putative Mit copy 1 nematode-resistance gene
9755	22893		2.14	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	28763	1.17	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	9.8E-01	AF174844.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3903	17062	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17062	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JMO883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JMO883
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JMO883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JMO883
7823	20876	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7823	20878	34379	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21895	35534	0.94	9.8E-01	P39652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23687		1.02	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33851	2.73	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.9	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35661	0.73	9.7E-01	BE799822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	BF511209.1	EST_HUMAN	UJH-B14-aci-e-07-O-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25789		3.17	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4556	17696	30675	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4556	17696	30676	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-F12 UM0053 Homo sapiens cDNA
5872	19082	32369	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2594
5872	19082	32370	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2594
6886	20038	33447	0.6	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7512	20588	34059	0.63	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8588	21887		1.52	9.6E-01	X95275.1	NT	P.falcatiparum complete gene map of plastid-like DNA (IR-A)
9052	22131	35875	0.92	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
11348	24408	38060	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11808	24798	38496	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG06 5'
11808	24798	38497	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG06 5'
12225	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centromeres protein 2 (CEP2), mRNA
12915	26081	31658	1.68	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15870	28794	1.81	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.5E-01	BE902340.1	EST_HUMAN	901675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	9.5E-01	BE902340.1	EST_HUMAN	901675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35819	0.71	9.5E-01	AI190162.1	EST_HUMAN	gd57d07.xt Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9308	22382	35833	1.04	9.5E-01	AW881102.1	EST_HUMAN	RC1-CT0295-24189-011-602 CT0295 Homo sapiens cDNA
11520	24578	38254	1.58	9.5E-01	BF218771.1	EST_HUMAN	901885103F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	9.5E-01	AW293799.1	EST_HUMAN	UH-B12-ahp-f03-0-UJ.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16445		6.72	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3289	16483		2.17	9.4E-01	AF080695.1	NT	Plasmodium falciparum zinc finger protein (ZFP1) mRNA, complete cds
9086	22145	35992	0.79	9.4E-01	M90724.1	NT	Human Fe-gamma-receptor IIA (FCGR2A) gene, exon 4
12498	25343		1.86	9.4E-01	BE781251.1	EST_HUMAN	901468703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868829 5'
12014	25975		1.4	9.4E-01	11418857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phyenyl-CoA hydroxylase (PHYH) gene, exon 5
2689	15818	28834	3.82	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4148	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4148	17298	30290	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5709	18802	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18988	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7496	20561		1.08	9.3E-01	AF270848.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	9.3E-01	AA847040.1	EST_HUMAN	ae09b03.st NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385557
9013	22092		1.1	9.3E-01	AF061981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35760	0.89	9.3E-01	AL161834.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	25583	31981	2.09	9.3E-01	11440298	NT	Homo sapiens insulin 1,4,6-triphosphate receptor, type 2 (TPR2), mRNA
13049	25588		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rL34 mRNA, complete cds
3311	19484	29505	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918184 3'
4899	18128		0.61	9.2E-01	BF129873.1	EST_HUMAN	601817814F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	19025		1.58	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (Zinc transporter), member 4 (Slc30a4), mRNA
6109	19289	32824	4.97	9.2E-01	BF037888.1	EST_HUMAN	601481153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6770	19925	33320	0.65	9.2E-01	M64703.1	NT	N. crassa valyl-tRNA synthetase (cyt-20/un-3) gene
9860	22800	36484	0.98	9.2E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22988	36582	1.31	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.5	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.64	9.2E-01	BF593251.1	EST_HUMAN	768606.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10883	23987	37698	1.78	9.2E-01	BE583811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
1654	14807	27892	1.52	9.1E-01	T96675.1	EST_HUMAN	601820312F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4052018 5'
2193	15328		1.49	9.1E-01	8823056	NT	ye5201.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element:
3275	18449	29468	1.28	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	18449	29469	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
6286	19469	32824	1.54	9.1E-01	L36033.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
6635	19794	33183	3.25	9.1E-01	DB1704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7750	20810	34300	17.46	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7816	20987	34473	2.61	9.1E-01	U72995.1	NT	cb71g08.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1338862 3'
10379	23414	37023	0.8	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12595	26054		19.67	9.1E-01	AF050113.1	NT	P80-COLLIN
3277	18451	29472	0.8	9.0E-01	7681523	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3439	19607		0.73	9.0E-01	AL161515.2	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4219	17368	33587	0.68	9.0E-01	8822310	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4498	17638	30620	1.43	9.0E-01	AF099810.1	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
5127	18252	31218	13.05	9.0E-01	AF017729.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
7951	20623	34100	0.82	9.0E-01	L42547.1	NT	Oryzobagus cuticular Rad51 (RAD51) mRNA, complete cds
7979	20651		1.42	9.0E-01	D38821.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
							Xenopus laevis gene for aldolase, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9549	22614	36183	0.68	9.0E-01	AF088761.1	NT	Danio rerio semaphorin Z1a mRNA, complete cds
10035	23073	36873	0.48	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25083	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5AR) gene, complete cds
5814	18004	32309	2.5	8.9E-01	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6378	19547	33134	1.28	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
6590	25827	33134	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	25827	33135	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.92	8.9E-01	AF269687.1	NT	Clithona nana cytochrome-c oxidase subunit 1 (cox1) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12423	25300	38766	4.02	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4684	17789	30788	2.11	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18688	31706	0.86	8.8E-01	AF310617.1	NT	Pseudorabies Virus Ea glycoprotein M gene, complete cds
7701	20768	34260	0.69	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7666978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEB), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	25072	38779	7.56	8.8E-01	AA808055.1	EST_HUMAN	bc38h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
12240	26158	38779	2.13	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
477	13672	26704	2	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2475	15602	28727	0.98	8.7E-01	5501883	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2838	16115	28127	5.32	8.7E-01	AA595863.1	EST_HUMAN	nm05f11.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18246		4.12	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
8229	21311	34831	0.66	8.7E-01	AW857335.1	EST_HUMAN	RC44NN0057-120500-013-007 NN0057 Homo sapiens cDNA
9130	22209	35752	0.66	8.7E-01	A1239456.1	EST_HUMAN	q336e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9130	22209	35753	0.66	8.7E-01	A1239456.1	EST_HUMAN	q336e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9809	22878	36569	2.07	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10511	23546	37156	1.08	8.7E-01	BF570193.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:4043564 3'
12034	25017	38721	3.32	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:4043564 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLOCYG07 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W69089.1	EST_HUMAN	zcd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3701	16871	29875	0.85	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S78772.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mouse, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7696	20761		0.84	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 125 of 172 of the complete genome
12856	25883		2.11	8.5E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.46	8.5E-01	AL111624.1	NT	Arabidopsis thaliana (ecotype Columbia) sp2 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7694	20759	34243	2.36	8.5E-01	BE542612.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8180	21262	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8613	21693	35230	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35315	0.68	8.5E-01	AL243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10558	23593	37198	1.49	8.5E-01	AB006799.1	NT	Cyandium calidarium gene for SigC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006799.1	NT	Cyandium calidarium gene for SigC, complete cds
12577	26056		5.29	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30989	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7891	21041	34553	0.57	8.4E-01	AF051142.1	NT	Mammalia brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
760	13941	26986	2.17	8.3E-01	M69437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
6383	18585	31494	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
8870	22910		4	8.3E-01	AI791952.1	EST_HUMAN	nm01112.6 NCL_CGAP_Cos8 Homo sapiens cDNA clone IMAGE:1076405 5' similar to contains THR11 THR repetitive element
10318	23351	36958	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000803.1	NT	Methanobacterium thermoautotrophicum from basos 1270510 to 1283409 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	8.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	15249	28369	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2166	15292		1.32	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2744	15861		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0974 protein, partial cds
4247	17393	30391	0.7	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
5217	18338	31311	1.19	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	18936	33332	0.59	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6781	18936	33333	0.59	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6813	20228	33681	0.76	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
7037	20173	33695	3.19	8.2E-01	AW376433.1	EST_HUMAN	CNA4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7416	25944	33966	4.48	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL 1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35258	0.55	8.2E-01	BE263145.1	EST_HUMAN	60114485F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23266	36956	0.81	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
10284	23289	36997	1.51	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10428	23483	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23483	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10596	23631	37269	3.78	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10596	23631	37240	3.78	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631	4.72	8.2E-01	L10127.1	NT	Mollusca contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013	38715	5.12	8.2E-01	P10983	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87388.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8109weeks_2N6HP8109W Homo sapiens cDNA clone IMAGE:252195.5'
12607	25408	32046	3.01	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2817	15931		1.38	8.1E-01	AF181839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	29723	2.77	8.1E-01	AF050568.1	NT	Homo sapiens MHC class 1 region
3547	16712	29724	2.77	8.1E-01	AF050568.1	NT	Homo sapiens MHC class 1 region
4730	17865	30847	0.63	8.1E-01	4606280	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
5825	19015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6445	19612	32975	0.89	8.1E-01	U16790.1	NT	(MELANOCORTIN-1 RECEPTOR) (MC1-R)
6759	19915	33309	2.17	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6759	19915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7681	20746	34227	0.7	8.1E-01	O47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							CYTCHROME B
8095	21177	34893	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8095	21177	34894	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8808	21887	35428	0.91	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	AF001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							xn01h03.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2692469.3' similar to SW:1YAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN. ;contains MER22.b1 PTR5 repetitive element;
8969	22048	35591	1.14	8.1E-01	AW242847.1	EST_HUMAN	PROBABLE E4 PROTEIN
10330	23395	36974	0.58	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10623	23657	37267	0.52	8.1E-01	N84541.1	EST_HUMAN	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KX9872.5' similar to EST (CLONE C-0PE11)
10769	23802		0.54	8.1E-01	AE001228.1	NT	Trepionema pallidum section 42 of 87 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38459	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
11772	24764	38480	2.82	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
12303	26221	32102	2.22	8.1E-01	AE001711.1	NT	Thermoboga maritima section 23 of 136 of the complete genome
181	13404		2.62	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
299	13516	26549	10.2	8.0E-01	AJ132772.1	NT	Bos taurus tub and rtf genes
2093	16233		1.86	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3146	16322	26334	1.32	8.0E-01	AF127897.1	NT	Samiti boliviensis olfactory receptor (SBO27) gene, partial cds
3387	16557	29572	1.29	8.0E-01	AB009103.1	NT	Mus musculus gene for ovalidial glycoprotein, complete cds
4655	17781	30775	6.77	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5098	18224	31196	1	8.0E-01	7657352	NT	Mus musculus myosin IXb (My9b), mRNA
8179	21261		2.86	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-406 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3'
10635	23660		0.48	8.0E-01	BE833326.1	EST_HUMAN	QV3-OT0065-280600-250-c08 OT0065 Homo sapiens cDNA
10927	23660	37483	0.48	8.0E-01	AB045597.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24267	37602	1.43	8.0E-01	Q92793	SWISSPROT	CREB-BINDING PROTEIN
468	13661	26697	0.75	7.9E-01	D11478.1	NT	Lymantia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 99 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1887	14839		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 64 of 163 of the complete genome
2337	15468	28603	9.03	7.9E-01	AB004816.1	NT	Oryzobagus cuticular mRNA for mitaumin28, complete cds
2338	15468	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3806	16769	28784	3.57	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17557		0.87	7.9E-01	BE263612.1	EST_HUMAN	801182033F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3635785 5'
4734	17669	30862	0.84	7.9E-01	6753746	NT	Mus musculus embigin (Emb), mRNA
4734	17669	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.68	7.9E-01	6753753	NT	Mus musculus embigin (Emb), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5235	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.66	7.9E-01	AF139718.1	NT	Chrysonya bezziana peritrophin-48 precursor, gene, complete cds
6479	19042	33003	0.68	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34903	2.68	7.9E-01	X80998.1	NT	P. salivum GR gene
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10255	23290	36887	5.43	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10298	23331	36834	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKc Homo sapiens cDNA clone GKCDRE12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10845	23878	37498	0.61	7.9E-01	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11286	24325		1.75	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein [KIAA1072], mRNA
11487	24546	38218	1.94	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
889	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2349	15480	28612	6.99	7.8E-01	AW959587.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17656	30842	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5h1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW763353.1	EST_HUMAN	RC3-CT0284-130100-023-c02 CT0284 Homo sapiens cDNA
6194	19370	32721	2.26	7.8E-01	AF116856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P06231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6591	19751	33136	0.84	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8688	21768	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	715405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D.discoideum racGAP gene
9533	22598	36170	0.56	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (NUP214), mRNA
10329	23364		1.28	7.8E-01	Q28452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	L28260.1	NT	Arabidopsis thaliana 1-amine-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	26403	5.78	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	13925						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II>
2776	15892	29003	1.72	7.7E-01	AF050157.1	NT	CITRATE SYNTHASE
3438	16606		1.34	7.7E-01	Q33916	SWISSPROT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3689	16831	29859	0.89	7.7E-01	8393408	NT	Homo sapiens PRO1976 mRNA, complete cds
4518	17655	30843	3.86	7.7E-01	AF118085.1	NT	Colurnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30644	3.38	7.7E-01	AF199488.1	NT	Colurnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32159	3.38	7.7E-01	AF199488.1	NT	RAFFINOSE INVERTASE (INVERTASE)
5678	18872	32160	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19256	32587	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
10049	23087	36689	1.41	7.7E-01	R08800.1	EST_HUMAN	YF24002.s1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:127155 3'
12452	25317		0.68	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
			7.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	18399	32748	5.26	7.6E-01	AF069510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	18399	32749	5.26	7.6E-01	AF069510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6847	19808	33193	0.68	7.6E-01	P37838	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6900	18509	31501	0.74	7.6E-01	AI253399.1	EST_HUMAN	act14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6900	18509	31628	0.74	7.6E-01	AI253399.1	EST_HUMAN	act14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7198	20081	33472	0.84	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.6E-01	AF145793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PHL.P (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (P127) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34924	2.38	7.6E-01	6857752	NT	Mus musculus actin (Actin-pending), mRNA
8318	21400	34925	2.38	7.6E-01	6857752	NT	Mus musculus actin (Actin-pending), mRNA
8520	21801	35137	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21801	35138	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9187	22245	35789	1.33	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2d9, phenobarbital inducible, type a (Cyp2d9), mRNA
9478	22836	36100	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9478	22838	36101	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11839	24719	38411	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11839	24719	38412	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24995		2.78	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25157		8.21	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	28807	1.08	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7690	20755	34240	0.8	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	29354		5.2	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
11554	14318	27372	1.61	7.4E-01	AI599146.1	EST_HUMAN	tn14b09.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2419	15548	28876	0.97	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3820	16980	29983	0.97	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17187	30175	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4429	17569	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4164340 5'
8910	21988		1.45	7.4E-01	U87060.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9298	22374	35925	6.88	7.4E-01	BE747503.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9357	22432	36990	1.24	7.4E-01	AA187986.1	EST_HUMAN	z467h01.s1 Stratiogene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:825297 3' similar to SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT
10613	22647	37256	0.7	7.4E-01	11424933	NT	Homo sapiens NY-REN-43 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12287	25213		1.7	7.4E-01	AI472841.1	EST_HUMAN	tat3h01.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		0.73	7.3E-01	AF000062.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4738	17873	30856	0.8	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	25841	33771	0.93	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7817	20687	34183	0.89	7.3E-01	Z14133.1	NT	D.melanogaster Cdc mRNA for clathrin heavy chain
7718	20782	34288	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7718	20782	34289	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38449	3.28	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.88	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	N.tubacum Nef-4A13 mRNA
2532	15557	28781	1.98	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	28323	1.27	7.2E-01	AF198100.1	NT	Fowpox virus, complete genome
3541	16705	28717	2.36	7.2E-01	AF068606.1	NT	Giardia intestinalis variant-specific surface protein (vsp-417-6) gene, vsp-417-6(A)-I allele, complete cds
3702	18863	28868	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3975	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108083.1	NT	Homo sapiens IA-2 gene, intron 18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4892	18022	31007	2.68	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5225	18347	31318	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
5308	18425	31395	0.85	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7382	20441	33903	0.59	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35285	1.31	7.2E-01	AF238081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241		0.54	7.2E-01	AF743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10548	23593	37192	2.25	7.2E-01	BF870061.1	EST_HUMAN	602118381F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4275381 5'
10977	24056	37690	3.28	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome c mRNA, complete cds
12630	18491	31530	1.51	7.2E-01	U02568.1	NT	Dicoryctes viviparus nematode polypeptide precursor (Dva) mRNA, complete cds
12787	25488		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
12784	26075		1.46	7.2E-01	Y10188.1	NT	B.thuringiensis PK1 & cap genes, putative
710	13892	28928	11.37	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3130	16308	28920	16.1	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4324	17467	30453	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4324	17467	30454	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6089	19251	32579	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6089	19251	32580	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7088	20182	33506	6.48	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
8934	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
8934	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
10058	23087	36700	1.6	7.1E-01	BE004405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10058	23087	36700	1.6	7.1E-01	BE004405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10621	23955	37285	1.1	7.1E-01	M12861.1	NT	Human T-cell receptor gamma chain J2 gene
12505	25958		2.64	7.1E-01	AA421492.1	EST_HUMAN	z06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27479	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15847	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07 s1 Soares multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2521	15647	28771	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5169	18291		2.32	7.0E-01	AL103301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	18255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8673	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1693 section 143 of 400 of the complete genome
9517	22592	36180	0.58	7.0E-01	U63868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9517	22592	36151	0.58	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13133	25937	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.9E-01	U69874.1	NT	Candida albicans equalase epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27666	2.91	6.9E-01	AA593530.1	EST_HUMAN	nr28a09.s1 NCI CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	16465	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3331	16696	29707	16.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868043 5'
5802	19091	32405	0.82	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BBN3 mRNA for notochord actin, complete cds
6112	19282	32627	0.85	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19696	33029	1.12	6.9E-01	BE295188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7979	21028	34542	0.58	6.9E-01	AF248883.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21250	34769	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9006	22836	36520	0.66	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9896	22836	36521	0.66	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10019	23653	37263	0.78	6.9E-01	BF242367.1	EST_HUMAN	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11536	24552	38268	2.11	6.9E-01	D89013.1	NT	601880580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11536	24552	38269	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12148	25949		3.77	6.9E-01	Q99958	SWISSPROT	Homo sapiens DAN gene, complete cds FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14152	27212	1.64	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2739	15856		1.41	6.8E-01	D90817.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2890	14798	27883	1.43	6.8E-01	AA654475.1	EST_HUMAN	aj7505.a1 Soares parathyroid tumor NHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gbX56411.maf ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4694	17829	30815	1.32	6.8E-01	J00762.1	NT	Raf(hooded) prolactin gene: exon iii and flanks
4980	18109	31085	0.82	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
9639	22878	36460	1.06	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23602		5.72	6.8E-01	AA687936.1	EST_HUMAN	nt13007.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gbX13546.maf1 Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38058	2.4	6.8E-01	AJ276675.1	NT	Siagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Siagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11376	24437	38008	1.91	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11376	24437	38097	1.91	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24633	38312	1.57	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11908	24893	38594	1.87	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial
11908	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial
309	13525	26559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13590	26588	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1961	15104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2214	15348	28477	1.88	6.7E-01	AA451884.1	EST_HUMAN	ZX12g12.s1 Soares total fetus Nb2HF8.9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TARI repetitive element
2235	16058	28498	5.16	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	16236	29258	5.81	6.7E-01	6675580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30986	0.62	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
5626	18820	31894	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5626	18820	31895	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	19265	32594	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6463	19620	32983	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6463	19620	32984	1.3	6.7E-01	9635036	NT	Gallid herpesvirus 2, complete genome
6764	19910	33304	0.59	6.7E-01	BE966241.2	EST_HUMAN	601690177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6764	19910	33305	0.59	6.7E-01	BE966241.2	EST_HUMAN	601690177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7495	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11196	24265	37900	2.06	6.7E-01	BF354649.1	EST_HUMAN	Human placental protein 14 (PP14) gene, complete cds
11746	23932	37558	2.76	6.7E-01	O14357	SWISSPROT	N-ACETYL GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
11959	24944	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
2670	15695	28319	0.97	6.6E-01	AF075240.1	NT	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2765	15680	28369	1.13	6.6E-01	AF198339.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
3578	16743	29760	1.16	6.6E-01	4506880	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3748	16908	29913	4.58	6.6E-01	Y07669.1	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
						NT	Calbicans random DNA marker, 282bp
4225	17373		2.48	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	19629	32990	3.82	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7272	20355	33808	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33809	0.62	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7862	20916	34421	3.7	6.6E-01	AV660508.1	EST_HUMAN	AV660508 GLC Homo sapiens cDNA clone GLCGD04 3'
8764	21843	35384	0.58	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9865	22905		2.34	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.6E-01	AU118188.1	EST_HUMAN	AU118188 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
640	13825	26848	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	26849	2.02	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3519	16855	29896	5.5	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30621	7.71	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18296	31258	2.88	6.5E-01	U28821.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5559	25807	31795	1.86	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
6865	20017	33426	1.3	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7760	20810	34309	0.74	6.5E-01	X04789.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7846	20901	34404	0.99	6.5E-01	A176882.1	EST_HUMAN	uc46902.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321842 3'
10042	23080		0.86	6.5E-01	T78904.1	EST_HUMAN	y221b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23977	37186	2.53	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10866	23964	37583	2.55	6.5E-01	H87593.1	EST_HUMAN	wt1706.r1 Soares_placenta_8to9weeks_ZNBP8c9W Homo sapiens cDNA clone IMAGE:282615 5'
10925	24008	37643	2.98	6.5E-01	AA601287.1	EST_HUMAN	not5c07.s1 NCL_CGAP_P1a1 Homo sapiens cDNA clone IMAGE:1100748 3'
11030	24109		3.38	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11899	24887	36586	5.43	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12566	25386		8.69	6.5E-01	BE465050.1	EST_HUMAN	h74410.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12840	25889		3.83	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL097c
262	13481	26513	8.59	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dyrelin light chain mRNA, complete cds
3546	16710	29721	4.42	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3994	17122	30125	1.46	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	M. musculus whn gene
4614	17751	30732	0.74	6.4E-01	Y12488.1	NT	M. musculus whn gene
6812	21691	36432	1.58	6.4E-01	AE001247.1	NT	Trepone pallidum section 63 of 87 of the complete genome
10221	23257		0.5	6.4E-01	11418320	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10284	23329	36933	7.31	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10309	23344	36949	1.31	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12693	25461		19.63	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
447	13643	26682	3.76	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
548	13741	26765	1.85	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2230	15364	28493	3.29	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2846	15789	28884	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2846	15769	28885	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.93	6.3E-01	Y12725.1	NT	Lycopodium esculentum p68a gene, complete cds
6189	19365	32713	0.84	6.3E-01	BE069306.1	EST_HUMAN	PMO-BT0767-010500-002-005 BT0767 Homo sapiens cDNA
6733	19889	33281	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19889	33282	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21708		3.44	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9087	22166	35712	0.79	6.3E-01	SE2927.1	NT	glycoprotein Ila (Alu 1 and 3' fusion junction) [human, Genomic Mutant, 300 nt]
9421	22495	36062	0.66	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9820	22675	36245	3.14	6.3E-01	9827521	NT	Varicella virus, complete genome
9820	22675	36246	3.14	6.3E-01	9827521	NT	Varicella virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	23673	37285	1.59	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1685 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW765395.1	EST_HUMAN	PM0-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24378	38024	1.78	6.3E-01	AA877745.1	EST_HUMAN	nc0806.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002916 HLARK.
11820	24671	38359	6.18	6.3E-01	A1904160.1	EST_HUMAN	QM-BT043-090299-046 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INOT-IDS2 INTERGENIC REGION
11888	24876	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.3 KD PROTEIN IN YMA12-APN1 INTERGENIC REGION
12086	25066	38772	1.47	6.3E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12358	25257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12582	26029		4.27	6.3E-01	X83528.1	NT	C. limicola pscD gene
6991	19179	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7654	20731		3.59	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Carr-r4) mRNA, partial cds
7715	25852	34266	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Catractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185
8487	21578	35114	4.97	6.2E-01	H72255.1	EST_HUMAN	ys01608.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP ⁺ oxidoreductase gene, complete cds
9848	21091	34606	1.47	6.2E-01	BE582887.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9710	22759		2.58	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10283	23318	36919	6.83	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23461	37067	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Sheb-related subfamily, member 1 (KCNB1), mRNA
10426	23461	37068	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Sheb-related subfamily, member 1 (KCNB1), mRNA
10756	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10758	23789	37408	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2468	15595		6.27	6.1E-01	6678078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5953	18847	32129	1.33	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CelYcd (hlt-1) alternatively spliced genes, complete cds
7009	20146	33564	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20146	33565	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20263	33736	0.87	6.1E-01	AW105653.1	EST_HUMAN	cd56h03.x1 NCL CGAP_OV23 Homo sapiens cDNA IMAGE:2567237 3' similar to gbX12871_mal HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); BY V-SRC)
7254	20337	33787	0.99	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033635.1	NT	Arabidopsis thaliana putative zinc transporter (ZTP1) mRNA, complete cds
8995	22074	35612	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8995	22074	35613	1.51	6.1E-01	11431066	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8915	22670	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
8915	22670	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36888	1.05	6.1E-01	AE004462.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 629 of the complete genome
10262	23287	36983	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23866	37489	0.47	6.1E-01	AF026993.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25695		1.16	6.1E-01	X95287.1	NT	M. mazai oriA, oriB, and oriC of archaeal ABC-transporter system
507	13701	28730	1.78	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
578	13787		4.74	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27823	1.83	6.0E-01	AF065263.1	NT	Human respiratory syncytial virus strain CH63-53b attachment protein (G) gene, complete cds
3917	17078	30073	0.87	6.0E-01	AJ233398.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv L genes, French strain 07-71
4305	17448		1.28	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5395	18697	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	UHLB1-seb-a-10-0-U1.s1 NCL CGAP_S033 Homo sapiens cDNA clone IMAGE:2718619 3'
5669	19828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
8900	19955	33355	0.88	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6956	20268	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6955	20268	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	6.49	6.0E-01	AL277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23066	36664	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01487	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
10594	23629		0.61	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0094-190700-017-d08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38529	2.74	6.0E-01	AI420623.1	EST_HUMAN	10807 x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE2095621 3'
12663	25440	32052	2.08	6.0E-01		EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.46	6.0E-01	AA706087.1	EST_HUMAN	388905.s1 Scores_fetal_liver_aplees_INFLS_S1 Homo sapiens cDNA clone IMAGE462778 3'
12953	25956		1.44	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12998	25933	31768	5.46	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25880		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14193	27254	1.09	6.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	15515	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	15516	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17450		3.95	5.9E-01	AF182756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5289	18407	31374	0.96	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	19754	33140	1.95	5.9E-01	AF085440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33992	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7556	20628		0.63	5.9E-01	X68801.1	NT	G. gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34795	0.48	5.9E-01	D0001.1	NT	Synochocystis sp. PCC5803 complete genome, 13/27, 1576593-1719843
8839	21918	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds
10117	23155		0.64	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10391	23426	37033	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10908	23991	37624	2.24	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23998	37632	1.71	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XP-TP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AW837176.1	EST_HUMAN	PM1-DT0041-190100-002-103 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/El CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.79	5.9E-01	L42320.1	NT	Oryzidegus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus niger pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12799	25533		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.26	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.9E-01	BF995738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4637	17773	30763	3.59	5.9E-01	AB003077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4817	18047		2.22	5.9E-01	AF110848.1	NT	Megascella scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5490	18089		1.02	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 56 of the complete genome
5648	18642	32123	0.81	5.9E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.9E-01	D78659.1	EST_HUMAN	HUM500508B Human placenta polyA+ (TFujivara) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32972	0.88	5.9E-01	D60601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6952	20285		2.37	5.9E-01	S86081.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.9E-01	H41571.1	EST_HUMAN	gb:S78187 M-Phase INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34878	0.66	5.9E-01	A1280051.1	EST_HUMAN	qh85510.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8278	21360	34879	0.66	5.9E-01	A1280051.1	EST_HUMAN	qh85510.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21468	34991	2.71	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP86
8385	21469	34992	2.71	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9092	22171	35716	10.4	5.9E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9172	22250	35793	1.23	5.9E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9173	22251	35794	0.57	5.9E-01	Q20471	SWISSPROT	POTENTIAL CASEIN KINASE I F46F22 IN CHROMOSOME X
9795	22835		0.79	5.9E-01	BF031608.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11237	24306	37943	7.26	5.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11291	24367		3.35	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11407	24468		1.44	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16784		0.73	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Fv1), mRNA
3295	16469	26488	1.46	5.7E-01	Q9WTJ2	SWISSPROT	POTENTIAL TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3593	16757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana peaces-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	19652	33014	4.41	5.7E-01	BF039413.1	EST_HUMAN	601454962F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3856590 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	Z38c06.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Borhyis chineesa strain T-4 cDNA library under conditions of nitrogen deprivation
7941	20991	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (PSCR) (PEC REDUCTASE)
8157	21239		0.55	5.7E-01	AJ251835.1	NT	Mus musculus Kcrq1, Ltprc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37461	0.91	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12255	25192		1.28	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA
13025	26675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601554814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3689	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913457 5'
12272	25204	38362	1.39	5.6E-01	AA493535.1	EST_HUMAN	hg75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element:
12661	17146	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12690	25460		2.66	5.6E-01	P50305	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25755		3.64	5.6E-01	BF573929.1	EST_HUMAN	60213028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8393912	NT	Rattus norvegicus Prokaryotic Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2766	15881	28990	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2766	15881	28991	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2885	18161	28178	1.17	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog) like (SKIV2L), mRNA
3134	16310		1.57	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N255-HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3306	16480	28501	2.93	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3783	16944	29051	1.34	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5249	18370		1	5.5E-01	AF063866.1	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
5269	18388	31356	1.01	5.5E-01	U68097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7439	20516		0.74	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8676	21756	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0458-170200-590-505 HT0458 Homo sapiens cDNA
9689	23008		0.56	5.5E-01	U88415.1	NT	Crinean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23623	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST028935 Fetal brain, Stralagene (cat#939200) Homo sapiens cDNA clone HFBCC35
11406	24467	38132	1.84	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	26404	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
147	13372	26405	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0928 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
598	13788	26808	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsIA (gsIA) genes, complete cds; and unknown genes
1300	14456	27522	2.21	5.4E-01	AW896097.1	EST_HUMAN	QV4-NN0040-070400-160-cd4 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE02247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2329	15461	28594	2.82	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-dlox gene)
5774	18908	32289	0.83	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0300-030200-503-c10 CN0300 Homo sapiens cDNA
6320	19492	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE86692.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806080 3'
7490	20595	34035	1.86	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7490	20595	34038	1.96	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10165	23232		2.69	5.4E-01	BF572536.1	EST_HUMAN	60207645F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243600 5'
11334	24397	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11920	24608	38607	2.76	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24906	38608	2.79	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	A1858398.1	EST_HUMAN	w37g04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
529	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
2843	15957	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29066	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16498	29506	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted G-type lectin precursor (LSLCL) gene, complete cds
4327	17470		1.2	5.3E-01	U98687.1	NT	Myoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y6 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:740711 5'
5671	18905	32150	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:566112 5'
5671	18965	32151	0.95	5.3E-01	AA193672.1	EST_HUMAN	zr42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:566112 5'
5762	18954	32257	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e72c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5762	18954	32258	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e72c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
9105	22184		1.59	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
9156	22234	35779	0.76	5.3E-01	BF433966.1	EST_HUMAN	7e71c12.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element1;
9156	22234	35780	0.76	5.3E-01	BF433966.1	EST_HUMAN	7e71c12.x1 NCL_CGAP_L124 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element1;
10416	23451	37056	0.85	5.3E-01	A1954210.1	EST_HUMAN	w94502.x1 NCL_CGAP_Med15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11857	24845	38542	5.63	5.3E-01	BE662991.1	EST_HUMAN	601339687F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
12145	25958		1.73	5.3E-01	AA916053.1	EST_HUMAN	q330e05.s1 NCL_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
839	14017	27072	20.65	5.2E-01	L20770.1	NT	APOLIPROTEIN D PRECURSOR (HUMAN); Drosophila melanogaster helix-loop-helix mRNA, complete cds
1190	14352	27410	7.57	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1218	14378	27438	3.05	5.2E-01	AF22492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1935	15078		3.88	5.2E-01	AI163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1935	15078		3.88	5.2E-01	AI163285.2	NT	Homo sapiens chromosome 21, segment HS21C085

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2213	16347	28478	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16384	28369	2.1	5.2E-01	U85942.1	NT	Chlamydomonas abortus strain S263 POMIP91A and POMIP90A precursor, genes, complete cds
3309	16483		1.05	5.2E-01	D73443.1	NT	Azobacter Vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3491	16558		1.61	5.2E-01	AL116780.1	NT	Butyris chinea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16695	29706	2.01	5.2E-01	AA084165.1	EST_HUMAN	am77605.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1016504 3'
3722	16893		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast mellea dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16895	29891	0.87	5.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4729	17894	30848	0.61	5.2E-01	6752847	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5770	19882	32263	0.92	5.2E-01	AA284261.1	EST_HUMAN	2a44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9832	25892	36562	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9932	25882	36563	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	2q05b09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:828783 5'
10233	23288	36858	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25736		4.83	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13817	26841	2.5	5.1E-01	M58909.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
665	13851	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pt vt1) 16S rRNA gene
1684	14836		1.02	5.1E-01	X87988.1	NT	R.norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	A1858495.1	EST_HUMAN	w39b12x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17446	30432	2.89	5.1E-01	P98380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541068.1	EST_HUMAN	601083608F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6406	19575		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAUF07 5'
7057	20110	33528	1.35	5.1E-01	R80873.1	EST_HUMAN	y94a08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
8770	21849	35389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8770	21849	35390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9886	22926	36510	4.65	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9889	22929	36513	3.95	5.1E-01	W22302.1	EST_HUMAN	55B1 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94879.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49	5.1E-01	BF030207.1	EST_HUMAN	80156883F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828787 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
12634	25427		1.31	5.1E-01	BF439982.1	EST_HUMAN	nc51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3408216 3' similar to contains element TAR1 repetitive element;
2203	15338	28464	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AF161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01	U65574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01	L38483.1	NT	Rattus norvegicus lagged protein mRNA, complete cds
3977	17134	30137	2.67	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19937		0.82	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21949	35484	0.66	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9657	21100	34613	2.13	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
9824	22894	36445	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4'-4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22894	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4'-4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10602	23637		1.23	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846436 5'
12307	25225		3.84	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13093	25713		2.25	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13981	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13991	27045	1.83	4.9E-01	BF571482.1	EST_HUMAN	602076949F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1692	14844	27928	1.08	4.9E-01	AJ243935.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28198	1.34	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61584	SWISSPROT	FIBRILLIN 1 PRECURSOR

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	18337	32682	2.87	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	18337	32683	2.87	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7910	20680	34156	1.81	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.86	4.9E-01	Q10608	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8180	22288		1.96	4.9E-01	BF209781.1	EST_HUMAN	601874984F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102803 5'
8389	22484	36028	0.96	4.9E-01	AW339905.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807286 3' similar to TR:095714
8498	26228		2.2	4.9E-01	10946863	NT	Q95714 HERC2 ;
10524	23559	37166	1.05	4.9E-01	AF033980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
12187	26154		2.61	4.9E-01	AF176912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
13085	26174		4.94	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13084	25714	31939	1.69	4.9E-01	AL163301.2	NT	nc22811.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144652 3'
13181	25788		1.27	4.9E-01	11431438	NT	Homo sapiens chromosome 21 segment HS21C101
4452	17592		0.69	4.8E-01	4504850	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
5624	18818	31892	9.66	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6817	19970	33378	0.89	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6827	19980		4.18	4.8E-01	AA659878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
7469	20544		1.83	4.8E-01	5031650	NT	nu85f08.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217613
7845	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (DRS2298E) mRNA
7938	20988	34487	3.69	4.8E-01	AL161482.2	NT	Homo sapiens chromosome 21 segment HS21C009
7938	20988	34498	3.59	4.8E-01	AL161482.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8089	21171	34886	1.81	4.8E-01	AB20744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
9446	22562		1.06	4.8E-01	BE156148.1	EST_HUMAN	y7710.y6 Soares breast 2NBRHBst Homo sapiens cDNA clone IMAGE:154785 5' similar to contains element MER6 repetitive element ;
10212	23248		0.55	4.8E-01	BF568633.1	EST_HUMAN	PM1-HT0380-201299-004-b04 HT0380 Homo sapiens cDNA
10866	24047		1.9	4.8E-01	X83602.1	NT	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
12279	25208		1.58	4.8E-01	AL163227.2	NT	S. cerevisiae ORFs from chromosome X
12509	25918		5.78	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
3142	16318		0.59	4.7E-01	AF192387.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6844	19803	33190	8.07	4.7E-01	BF217173.1	EST_HUMAN	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
7186	20051	33461	0.84	4.7E-01	AI204374.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
							q172a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22352	35904	0.61	4.7E-01	6991501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk57697 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 8 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW88948.1	EST_HUMAN	RC6-N10028-240400-011-E08 N10028 Homo sapiens cDNA
12401	25281		1.84	4.7E-01	BE887783.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_81 Homo sapiens cDNA clone IMAGE:2809198 3'
3837	16997	29999	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.62	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5535	18732	31747	0.93	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5535	18732	31748	0.93	4.6E-01	BF131593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5588	18783	31828	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829	3.52	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5653	18857	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568759F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5677	18871	32157	3.62	4.6E-01	AL247679.1	EST_HUMAN	qt159h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN ;
5677	18871	32158	3.62	4.6E-01	AL247679.1	EST_HUMAN	qt159h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN ;
5685	18879	32169	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOR1
5763	19055		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from basas 1165761 to 1176238 (section 100 of 148) of the complete genome
6906	20221	33649	2.39	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25543	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegalovirus a1 protein gene, complete cds
7906	20958	34464	0.78	4.6E-01	AA493577.1	EST_HUMAN	rh04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943363 similar to contains Alu repetitive element; contains element L1 repetitive element ;
8515	21696	35131	14.55	4.6E-01	BF697399.1	EST_HUMAN	602130955F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4287828 5'
8946	22025	35565	0.54	4.6E-01	AA932237.1	EST_HUMAN	cc076b08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	22025	35566	0.54	4.6E-01	AA832237.1	EST_HUMAN	cc78b08.s1 NCI CGAP_K45 Homo sapiens cDNA clone IMAGE:1572087.3' similar to gb:M36341 ADP- RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9868	22806	36490	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9868	22806	36491	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23218	36809	1.16	4.6E-01	A015634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766.3'
10181	23218	36810	1.16	4.6E-01	A015634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766.3'
11238	24307		2.31	4.6E-01	P98163	SWISSPROT	PULATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11248	24317	37858	5.08	4.6E-01	BE185448.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37857	5.06	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.6E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.6E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	15103	28203	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2633	16110	29124	4.83	4.5E-01	AA677086.1	EST_HUMAN	z55d02.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179.3'
3380	16552	29565	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885280.3' similar to gb:L07807
3380	16552	29566	0.68	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI CGAP_Co19 Homo sapiens cDNA clone IMAGE:2885280.3' similar to gb:L07807
3393	16583	29578	4.46	4.5E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3465	15532	29651	1.51	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4139	17291		1.18	4.5E-01	Q28247	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4188	17336	30329	1.02	4.5E-01	A1708908.1	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4292	18478		4.71	4.5E-01	AW873495.1	EST_HUMAN	as55e09.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480.3'
5058	18186	31161	1.18	4.5E-01	BE863445.2	EST_HUMAN	hcd0g02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810.3'
5668	18860	32146	1.67	4.5E-01	AW608814.1	EST_HUMAN	601857228R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886023.3'
6740	18896		1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7571	20843	34120	0.91	4.5E-01	M37036.1	NT	COAT PROTEIN
							Rat nuclear proteins B23.1 and B23.2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7785	20841	34333	2.39	4.5E-01	A186849.1	EST_HUMAN	w132602.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8502	21583		1.11	4.5E-01	M32661.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT ; D melanogaster Shaw2 protein mRNA, complete cds
8598	21679	35217	2.87	4.5E-01	A1848596.1	EST_HUMAN	1256g11.x1 NCL CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3'
8756	21835	35376	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE) Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
8981	22060		2.36	4.5E-01	11444786	NT	Escherichia coli K-12 MG1685 section 108 of 400 of the complete genome
9200	22278	35617	0.86	4.5E-01	AE000218.1	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10145	23183		0.96	4.5E-01	9630816	NT	EST02631 Fetal brain, Striatum (cat836206) Homo sapiens cDNA clone HFBCY17
10713	23746	37352	25.59	4.5E-01	M86006.1	EST_HUMAN	EST02631 Fetal brain, Striatum (cat836206) Homo sapiens cDNA clone HFBCY17
10713	23746	37353	25.59	4.5E-01	M86006.1	EST_HUMAN	EST02631 Fetal brain, Striatum (cat836206) Homo sapiens cDNA clone HFBCY17
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	Q04262 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]
11225	24294	37835	2.16	4.5E-01	11430799	NT	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11530	24595		1.3	4.5E-01	AV718382.1	EST_HUMAN	AV718382 GLC Homo sapiens cDNA clone GLC0212 5'
12164	26182		5.58	4.5E-01	BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852961 5'
12895	25592		1.2	4.5E-01	BF33753.1	EST_HUMAN	602035275F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183280 5'
12970	25630		12.42	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2094	15234		1.11	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (limap1), mRNA
2462	15589	28715	4.16	4.4E-01	P48765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3390	16560	28675	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	28676	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	16565	29580	2.12	4.4E-01	BF056726.1	EST_HUMAN	7191d02.y1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3383795 5'
4349	17492		1.35	4.4E-01	BE378707.1	EST_HUMAN	601237193F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603993 5'
5336	18733	31749	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5338	18733	31750	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	S65019.1	NT	mucln [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013	32319	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLC05C12 5'
6074	19256	32584	1.12	4.4E-01	AI198413.1	EST_HUMAN	q182h11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q82h11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
6370	19339	32899	1.67	4.4E-01	AW080795.1	EST_HUMAN	xc27c08.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685510 3' similar to TR:Q95164 Q95154 AFLATOXIN B1-ALDEHYDE REDUCTASE ;
6458	19825		1.05	4.4E-01	AA776132.1	EST_HUMAN	ae85d11.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN);
7697	20628	34104	1.14	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)
8982	22041	35984	1.11	4.4E-01	AA056427.1	EST_HUMAN	z69a03.s1 Striatagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
9352	22427	35985	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9395	22460	36023	0.62	4.4E-01	AW612578.1	EST_HUMAN	hiv5c08.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2654222 3' similar to
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	SW_MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
10167	23204	36798	1.95	4.4E-01	A128650.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	gc39f09.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10302	23337	36942	4.94	4.4E-01	P36590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10585	23620	37226	1.76	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23962	37486	0.46	4.4E-01	P02716	SWISSPROT	beta -HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11523	24578	38256	1.64	4.4E-01		NT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
12435	25308	32087	4.23	4.4E-01		NT	Tarbatulina retusa mitochondrion, complete genome
12447	26084		13.47	4.4E-01	AL163282.2	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
13051	25689		1.41	4.4E-01	P54725	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
424	13619	26659	2.42	4.3E-01	AF155218.1	NT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619	26660	2.42	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
1633	14785	27871	1.11	4.3E-01	AW86550.1	EST_HUMAN	Callitrix jacchus MW/LW opsin gene, upstream flanking region
2835	16112		1.34	4.3E-01	AW935289.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
3127	16303	29316	0.95	4.3E-01	AW999477.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4526	13619	26659	1.27	4.3E-01	AF155218.1	NT	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4526	13619	26660	1.27	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
5071	18199		1.04	4.3E-01	AL161502.2	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
5220	18342		0.94	4.3E-01	9635250	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5480	18678	31693	0.65	4.3E-01	P48634	SWISSPROT	Xestia c-nigrum granulovirus, complete genome
5480	18678	31694	0.65	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
			0.85	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6009	19194	32512	1.31	4.3E-01	BE181665.1	EST_HUMAN	QV1-HT0638-070500-191-c08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Salmir ecdureus olfactory receptor (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Columix columix japonica fnG gene
6825	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7586	20558		1.28	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4158286 5'
8622	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C1 (flaC-fla) genes, complete cds
9455	22571	36137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9928	22968	36556	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
9928	22968	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10433	23498	37076	0.99	4.3E-01	AW170589.1	EST_HUMAN	xt63605.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.56	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1388	16036	27618	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA761653.1	EST_HUMAN	nz24e09.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3697	16858	29862	4.1	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3727	16988	29892	1.09	4.2E-01	AI280338.1	EST_HUMAN	q94b01.x1 Soares_NHMPUL S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	18477		0.73	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40493
3984	17141	30146	0.74	4.2E-01	AW835627.1	EST_HUMAN	QV0-LT0015-180200-127401 LT0015 Homo sapiens cDNA
4819	17952	30937	2.57	4.2E-01	AA694093.1	EST_HUMAN	n69h01.s1 NCI CGAP Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	y777e01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5832	18023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5901	19090	32404	1.63	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0234-060400-029-g04 CT0254 Homo sapiens cDNA
6334	19505	32853	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7090	20184	33608	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7090	20184	33609	8.72	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7151	29839	33727	3.21	4.2E-01	S82504.1	NT	Brc1 breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7242	20323	33770	6.61	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, centig fragment No. 47
7745	20805	34294	0.81	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21284	34786	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8182	21284	34787	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9511	22578	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22578	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10175	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	z95601.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10714	23747	37364	1.44	4.2E-01	AW863666.1	EST_HUMAN	MF3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
11298	24364	38005	1.43	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11678	24678	38368	1.87	4.2E-01	BE968485.2	EST_HUMAN	601660352RT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906086 3'
1118	14283	27338	2.11	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210160-142 BT091 Homo sapiens cDNA
1127	14292	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2775	15890	28001	1.46	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3008	16181	28202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3008	16181	28203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29561	0.86	4.1E-01	AA906344.1	EST_HUMAN	q94508.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST1373364 MAGG resequences, MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST1373364 MAGG resequences, MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE and isoF genes
4422	17563		0.99	4.1E-01	AA909257.1	EST_HUMAN	on33602.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4789	17924	30912	1.36	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6111	19291	32626	4.84	4.1E-01	BF681393.1	EST_HUMAN	602156580F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287319 5'
6857	20010	33420	0.65	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine raties (Soyes6) gene, complete cds
7590	20661	34137	2.49	4.1E-01	U87635.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8226	21307	34827	1.36	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9282	22568	35918	1.51	4.1E-01	6755621	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpoc-pending), mRNA
9765	22762		0.75	4.1E-01	AF160597.1	NT	Vesicular glandularis Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10470	23505		1.98	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC1168 complete genome, segment 3/6
10822	23656	37266	1.15	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLCVD12 3'
10725	23768	37365	0.68	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK99)
10725	23768	37366	0.68	4.1E-01	P18594	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK99)
10806	23839		1.14	4.1E-01	BF349382.1	EST_HUMAN	GM2-HT0137-200969-010-e08 HT0137 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	X58700.1	NT	Zea mays ZMIPNS2 gene for 19 kDa zein protein
11075	23903	37525	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12810	26139		2.33	4.1E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1064	14229	27286	1.49	4.0E-01	8404856	NT	Lactuca rubellus mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2061	16053	28316	1.08	4.0E-01	Z96933.1	NT	Ascarobolus immerus msc2 gene
2061	16053	28317	1.08	4.0E-01	Z96933.1	NT	Ascarobolus immerus msc2 gene
2866	13369	26402	1.11	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
3033	16209	29231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	29232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (MIC), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3766	16947	29955	1.87	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4938	18088		8.59	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6031	19214	32535	1.07	4.0E-01	AW970610.1	EST_HUMAN	EST382891 IMAGE resequences, MAGK Homo sapiens cDNA
6668	19730	33108	0.62	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
8113	21195	34714	0.61	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
8201	21263	34806	0.73	4.0E-01	AB016626.1	NT	Homo sapiens OCTN2 gene, complete cds
9208	22286	35827	1.11	4.0E-01	A4323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11869	24857		1.67	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_B9 Homo sapiens cDNA clone IMAGE3828092 5'
12021	25005		2.38	4.0E-01	L76080.1	NT	Synochocystis sp. FCC 9413 transposase gene, complete cds
12463	26978		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
13027	26116		1.38	4.0E-01	Z49301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL026w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	hab84605.x1 Soares_NSF_P8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SW:NTCR_BOVIN_O18875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1;
13222	25907		1.28	4.0E-01	Z49301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL026w
1408	14563	27638	1.64	3.9E-01	AF206818.1	NT	Gorilla gorilla carboxyl-ester lyase (CEL) gene, complete cds
2707	15825	28940	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2770	15885	28994	5.03	3.9E-01	X82032.1	NT	H. sapiens B-myb gene

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2770	15995	28995	5.03	3.9E-01	X82032.1	NT	H sapiens B-myb gene
3168	16341	29349	4.24	3.9E-01	AJ225898.1	NT	Sinorhizobium meliloti egl_syrB2, oya3 genes and orf3
4160	17340	30333	1.48	3.9E-01	BF592611.1	EST_HUMAN	7861801.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339189 3'
5108	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:383369 5'
6055	19237	32562	4.58	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19579	32840	0.64	3.9E-01	U82685.2	NT	Homo sapiens zinc finger, protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.99	3.9E-01	U78415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-1) gene, complete cds
8062	22141	35886	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0106-170806-004-008 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	602019844F1 NCI_CGAP_Br167 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22509	36075	1.73	3.9E-01	AW166898.1	EST_HUMAN	602019844F1 NCI_CGAP_Br167 Homo sapiens cDNA clone IMAGE:4155322 5'
9745	22809	36387	1.59	3.9E-01	AI937337.1	EST_HUMAN	602019844F1 NCI_CGAP_Br167 Homo sapiens cDNA clone IMAGE:4155322 5'
10082	23120	36722	2.88	3.9E-01	MT9879.1	NT	Human diaphanin 27 gene, exons 10 and 11, and L1 and Alu repeats
10150	23188		0.58	3.9E-01	11465620	NT	Porphyra purpurea mitochondrion, complete genome
10369	23404	37015	0.92	3.9E-01	D80722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10582	23597	37203	0.61	3.9E-01	BF381856.1	EST_HUMAN	CM2-NN0034-030600-218-104 NN0034 Homo sapiens cDNA
10582	23597	37204	0.61	3.9E-01	BF381856.1	EST_HUMAN	CM2-NN0034-030600-218-104 NN0034 Homo sapiens cDNA
10838	23869		0.47	3.9E-01	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBCQC11 5'
12049	25030	38736	1.89	3.9E-01	AV702623.1	EST_HUMAN	AV702623 ADB Homo sapiens cDNA clone ADBBE06 5'
12221	26055		4.03	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12916	26503		1.75	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
518	13711		6.1	3.8E-01	AB029291.1	NT	Mus musculus pom-1 mRNA for pericardial material-1, complete cds
1919	15062		1.36	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 18 of 229 of the complete genome
2637	15700	28674	1.84	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2697	16069	28631	5.2	3.8E-01	6078002	NT	Mus musculus solute carrier family 1, member 8 (Slc1a8), mRNA
3066	16242		0.71	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 89SE-MIP1213)
3113	16289	29305	1.91	3.8E-01	AF043883.1	NT	Plasmodium falciparum aminopeptidase N (ampn) gene, partial cds
3572	16737	28752	8.7	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3628	16782		1.09	3.8E-01	AB072119.1	EST_HUMAN	602019844F1 NCI_CGAP_Br167 Homo sapiens cDNA clone IMAGE:2357855 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf36b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	6764085	NT	Mus musculus general transcription factor II (GTF2), mRNA
6727	18920	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	19636		0.63	3.8E-01	S46825.1	NT	p191 protein [mink, Genomic, 2446 nt]
6761	19917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-a02 BT0537 Homo sapiens cDNA
6896	20214	33844	4.39	3.8E-01	AI374601.1	EST_HUMAN	ts4f11.x1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains ALU repetitive element;
7079	20132	33649	1.38	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26
7685	20760		4.27	3.8E-01	X67597.1	NT	Mus musculus gene for kallikrein-binding protein
8493	21574	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8826	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22098	35638	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains ALU repetitive element; contains PTR5 repetitive element;
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11699	24696	36388	1.57	3.8E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), celltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11824	24813		2.87	3.8E-01	BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	36681	2.5	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977	36682	2.5	3.8E-01	R42550.1	EST_HUMAN	y62h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12569	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
13105	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31933	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	15876	28799	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3874	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MP3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18389	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18389	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens Interferon-induced protein p78 (MX1) gene, complete cds
6071	19253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19798	33187	0.7	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	19819		0.8	3.7E-01	L10383.1	NT	Mus scrofa haptoglobin mRNA, complete cds
7283	20375	33832	3.48	3.7E-01	11625843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7965	21015	34527	0.89	3.7E-01	T68802.1	EST_HUMAN	yaf0407.3 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:66324 5'
8524	21605	35143	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA902912.1	EST_HUMAN	ok43b11.s1 NCL CGAP_Lu2 Homo sapiens cDNA clone IMAGE:1518701 3'
8402	22476		1.34	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15-dioxygenase (BCDO gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10414	23449	37054	4.21	3.7E-01	A133641.1	EST_HUMAN	q46b07.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10783	23816	37437	0.46	3.7E-01	U08381.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08381.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11087	24170	37805	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37989	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11285	24351	37990	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37566	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12004	24989		1.42	3.7E-01	AA978540.1	EST_HUMAN	cc46403.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698
12066	25047		3.5	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12137	25954		1.17	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12314	25229		3.94	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	25289		1.82	3.7E-01	D86976.1	NT	Chlamydomonas psittaci partial omp1 gene for outer membrane protein 1
12821	25548		2.94	3.7E-01	AL121154.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12902	25697	31971	6.99	3.7E-01	Y18000.1	NT	DKFZp762K075.t1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762K075 5'
271	13489	26520	0.77	3.6E-01	AJ009609.1	NT	Homo sapiens NF2 gene
1020	14191		9.07	3.6E-01	U89241.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mibp gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	yf03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1886	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	yf03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1886	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
							hg33102.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28253	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	15251		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15530		2.8	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2556	15681	28306	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2694	15814	28929	1.69	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2884	16475		8.47	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3558	16723	29738	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3558	16723	29739	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4528	17656	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4863	17966	30981	0.69	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAPK4 alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW339393.1	EST_HUMAN	ha2g04.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5209	18330	31302	0.92	3.6E-01	BE087689.1	EST_HUMAN	MR2-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5498	18697	31713	0.84	3.6E-01	AJ008565.1	NT	Homo sapiens lipase gene intron 5
6211	19386	32735	0.96	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6607	19787	33155	1.63	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7298	20380		3.85	3.6E-01	R94090.1	EST_HUMAN	y74a06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:275987 5'
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	w72c10.x1 Soares thymus_NHfTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8419	21500	35032	0.75	3.6E-01	P88167	SWISSPROT	O15117 FYN BINDING PROTEIN, [1];
8474	21555	35087	16.45	3.6E-01	AL161583.2	NT	SCO-SPONDIN
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9179	22257	35799	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9393	22468	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9599	22654	36225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9599	22654	36226	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9669	22631		0.58	3.6E-01	X62825.1	NT	C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11187	24256	37891	2.42	3.6E-01	BE902390.1	EST_HUMAN	60167641BF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958897 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915	37540	4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens HHb5 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25287		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.98	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW160226.1	EST_HUMAN	X60611.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN
13146	25745		1.38	3.6E-01	Z54173.1	NT	ALPHA-1 CHAIN (HUMAN);
214	13437	26467	3.71	3.5E-01	6678933	NT	Pyrococcus sp. pol gene
695	13878	26911	1.03	3.5E-01	AL161581.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
743	13924	26965	1.53	3.5E-01	7706136	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26966	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13981	27033	4.66	3.5E-01	BF12976.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
1670	14822	27905	1.28	3.5E-01	U35776.1	NT	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
2671	16058	28908	1.34	3.5E-01	AA223252.1	EST_HUMAN	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
3795	16956		0.73	3.5E-01	BF214391.1	EST_HUMAN	z08a09.s1 Striatogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
4378	17521	30501	2.62	3.5E-01	AF071253.1	NT	601845470F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076890 5'
5048	18176	31153	4.34	3.5E-01	MT18349.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds
5323	13349	26376	0.6	3.5E-01	AL161536.2	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5449	18649	31627	1.1	3.5E-01	Q66687	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
5449	18649	31628	1.1	3.5E-01	Q66687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18681	32146	1.29	3.5E-01	D42045.1	NT	EARLY E2A DNA-BINDING PROTEIN
5667	18681		1	3.5E-01	AW1663916.1	EST_HUMAN	Human mRNA for KIAA0088 gene, complete cds
							PMA-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw79D3.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:762429 5' similar to TR:G1066935
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6803	19958	33358	0.9	3.5E-01	O24357	SWISSPROT	Bos taurus peptidyl methionine sulfoxide reductase (msrA) mRNA, complete cds
7201	20066		3.38	3.5E-01	X88505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (36PD)
7713	20778	34284	0.59	3.5E-01	P47281	SWISSPROT	S. scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34265	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8265	21347	34862	0.82	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8662	21742		0.77	3.5E-01	AF051561.1	NT	RC4-ET0024-280900-014-c07 ET0024 Homo sapiens cDNA
9127	22206	36749	1.17	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9937	22976	36597	1.75	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10090	23128	36731	4.78	3.5E-01	Z28825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	Xi laevis gene for albumin including HP1 enhancer
10372	24052	37685	2.62	3.5E-01	X51084.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11274	24342	37681	1.97	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
11274	24342	37682	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11892	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
11990	24965	38667	1.53	3.5E-01	L05145.1	NT	y280H12.r1 Soares multiple sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:290375 5'
12271	26209		1.51	3.5E-01	AF297468.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12344	26249		6.66	3.5E-01	X64565.1	NT	Schistosoma mansoni strain NMR1 chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12507	26348		2.91	3.5E-01	AE001774.1	NT	B. laurus atpA1 gene for F0(F1) ATP synthase alpha-subunit
12710	25472		1.5	3.5E-01	AE001681.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
13198	28026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermotoga maritima section 3 of 136 of the complete genome
13198	28026	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	y684f11.r1 Soares retina N2b4f-R Homo sapiens cDNA clone IMAGE:219997 6'
725	13907		1.78	3.4E-01	AJ242950.1	NT	y684f11.r1 Soares retina N2b4f-R Homo sapiens cDNA clone IMAGE:219997 5'
998	14169	27230	8.2	3.4E-01	Y09788.2	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	Pseudomonas fluorescens colR, colS genes, of222 and partial inaA gene
1357	14512	27585	2.35	3.4E-01	Y00554.1	NT	QV3-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
2474	15601	28726	2.54	3.4E-01	D90909.1	NT	Azobacter vinelandii nifA gene for NifA protein (positive regulatory element)
							Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3065	16241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3085	16241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16382	29403	1.09	3.4E-01	D90909.1	NT	Synschoecysis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16593	29608	0.78	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylothermus sp. strain SS1 putative GpE (gpe), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.89	3.4E-01	BF446010.1	EST_HUMAN	Tn94e01.x1 NCL_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15
4163	17313		1.48	3.4E-01	AA584196.1	EST_HUMAN	Q8UJ15 DJ18C8.1
4767	17802	30884	1.78	3.4E-01	BE069912.1	EST_HUMAN	nc11b10.st NCL_CGAP_Phen Homo sapiens cDNA clone IMAGE:1100347 3'
5066	18184		4.3	3.4E-01	A1240973.1	EST_HUMAN	MR4-BT0403-230200-202-01 BT0403 Homo sapiens cDNA
5802	18982	32295	2.64	3.4E-01	AL161594.2	NT	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5832	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02971.1	NT	zn12d11.st Stralagene NNT neuron (H837233) Homo sapiens cDNA clone IMAGE:947221 3'
6154	19330	32676	0.96	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204505.1	EST_HUMAN	901671811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6364	19634	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	UH-BH1-aet-e-12-0-JL:st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6882	20034		1.39	3.4E-01	N95226.1	EST_HUMAN	DKFp761A249.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFp761A249 5'
7066	20180	33604	1.07	3.4E-01	A1468082.1	EST_HUMAN	zb5e12.st Scaraes_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	tn63g05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
8090	21172		0.48	3.4E-01	AE000493.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.68	3.4E-01	Y14930.1	NT	602085233F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4249365 5'
8584	21764		1.38	3.4E-01	AA337083.1	EST_HUMAN	Echerichia coli K-12 MG1685 section 383 of 400 of the complete genome
8760	21839	35380	0.71	3.4E-01	L04690.1	NT	Homo sapiens TCRAV28 gene, allele A4, partial
9053	22132	35576	1.87	3.4E-01	P28013	SWISSPROT	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	Osteolus gireus cholesterol 7-alpha-hydroxylase gene, complete cds
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9821	22678		0.57	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9845	21088	34602	4.68	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
							Ephydaria fluviatilis mRNA for PLC-gamma5, complete cds
							Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9845	21088	34803	4.68	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1 p (MAF1) gene, complete cds
9897	22837	36522	0.86	3.4E-01	U68783.1	NT	Glycine max putative transcription factor SCOF-1 (scdf-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10695	23728		0.73	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11267	24338		3.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABILE E4 PROTEIN
11350	24412	38068	1.86	3.4E-01	AF045981.1	NT	Rattus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25858.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-globin/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF061948.1	EST_HUMAN	7k68d12x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:3480646 3'
12110	25080	38793	1.65	3.4E-01	Q27546	SWISSPROT	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)
12150	25120		2.03	3.4E-01	U63604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12264	25188		1.55	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
12367	25912		1.16	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf19p (cwf19) gene, complete cds
12489	25338		10.71	3.4E-01	L26539.1	NT	Human autotigen mRNA, complete cds
12517	25944		2.98	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12579	26032		1.79	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12700	26466	32023	1.38	3.4E-01	AJ297191.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
12954	26160		1.96	3.4E-01	AJ288948.1	NT	Clostridium cellulolyticum partial spoIVB gene and spoOA gene, strain ATCC 35319
13055	26891		2.26	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
13055	26891		2.26	3.4E-01	AF019413.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
108	13253	26253	6.72	3.3E-01	X07590.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
461	13656	26694	3.19	3.3E-01	X07590.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
650	13836	26863	1.97	3.3E-01	7552485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1227	14387	27450	2.57	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1335	14492	27562	3.39	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	14788	27873	1.28	3.3E-01	6753985	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1674	14928		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Rss recognition component (Krc), mRNA
1777	14928		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week Homo sapiens cDNA 5' and
2477	15604		6.23	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
3014	16190	29215	1.61	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (L-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus methylamylase biosynthetic genes
3584	16749	29766	1.04	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30068	2.72	3.3E-01	O84646	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30262	1.81	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17927		2.37	3.3E-01	D31692.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17945		1.91	3.3E-01	AI538114.1	EST_HUMAN	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4843	17976	30966	1.02	3.3E-01	M24461.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
4930	18089	31065	1.14	3.3E-01	D64003.1	NT	R. norvegicus mRNA for 3' UTR of ubiquitin-like protein
5439	18639	31617	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3' UTR of ubiquitin-like protein
5439	18639	31618	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3' UTR of ubiquitin-like protein
5907	19096	32411	0.68	3.3E-01	BF213673.1	EST_HUMAN	601848030FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6087	19249	32576	1.37	3.3E-01	BE819650.1	EST_HUMAN	601472768T NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6087	19249	32577	1.37	3.3E-01	BE819650.1	EST_HUMAN	601472768T NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6182	19338	32684	1.29	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6932	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter lilioralis gybB gene for DNA gyrase B subunit, partial cds
6932	20247	33681	0.59	3.3E-01	AB034233.1	NT	Flexibacter lilioralis gybB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	ly64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	ly64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7961	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21838	35379	23.1	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22390	35941	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9378	22720	36280	1.16	3.3E-01	BE5828481.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9578	22720	36290	1.16	3.3E-01	BE5828481.1	EST_HUMAN	CM3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	N69866.1	EST_HUMAN	zab7h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9752	22690	36260	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233	37620	2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10865	23897	37620	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37675	3.35	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
10960	24041	37675	3.35	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
11279	24345	38242	2.1	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11607	24565	38242	9.36	3.3E-01	BE219351.1	EST_HUMAN	hr57g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11826	24706	38399	3.7	3.3E-01	P47963	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-26) (CBP30)
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	db71g02.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338850 3'
12036	13253	26253	2.33	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5.J nodX gene
12250	25190	38357	1.85	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	26685		22.08	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (217)
469	13694		2.5	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
736	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14467	27535	1.48	3.2E-01	Z60202.1	NT	P. vulgaris arcs-1 gene
1421	14575	27648	6.74	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1653	14815		1	3.2E-01	AF208730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1823	14974	28080	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST366264 MAGC resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST366264 MAGC resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111685.1	NT	Bethylis chinensis strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2808	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx/mot11 homeobox (Pbxmot1), mRNA
2774	15889	29000	1.23	3.2E-01	AF060598.1	NT	Homo sapiens promyelocytic leukemia zho finger protein (PLZF) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3698	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.93	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4514	17653	30641	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4621	17758	30740	1.35	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL B1.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4860	17893		8.99	3.2E-01	BF683617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248505 5'
5386	18588	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CM0-H70569-060300-269-110 H70569 Homo sapiens cDNA
6078	19260	32589	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
6433	19601	32965	0.73	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c-
6729	19895	33277	0.65	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FH7A Homo sapiens cDNA clone FHTAABH01 5'
6872	20024		1.17	3.2E-01	AB002358.1	NT	Human mRNA for KIAA0381 gene, KIAA0381 protein
8040	21123	34643	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8365	21448	34069	1.5	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8461	21542	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12W/alpha1
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21646	35187	14.52	3.2E-01	BF311633.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8656	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8698	21778	36510	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	35311	0.69	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Deinoceratus radiolurans R1 section 152 of 228 of the complete chromosome 1
8871	21950	35485	0.88	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
8871	21950	35486	0.88	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9287	22344	35895	0.67	3.2E-01	AL163304.2	NT	Homo sapiens chromosome 21 segment HS21C004
9278	22354		2.54	3.2E-01	M86511.1	NT	Human monocytic antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 5-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10108	23235	36824	4.33	3.2E-01	U44814.1	NT	Borrelia burgdorferi plasmid p32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	h69105.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10518	23553		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stralagene (cat#8936206) Homo sapiens cDNA clone HFBDZ21
12289	26083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12861	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25669		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE385776.1	EST_HUMAN	601275480 F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616748 5'
2736	15853	28967	3.39	3.1E-01	R18051.1	EST_HUMAN	y60106 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2762	16001	28985	3.77	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2762	16001	28986	3.77	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2920	16098		1.28	3.1E-01	AW620036.1	EST_HUMAN	h146h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3242	16416		3.51	3.1E-01	AB020069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
4016	17173	30181	0.94	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5077	18205	31177	0.7	3.1E-01	AE003964.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5595	18790	31838	9.24	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1236
5718	18911	32206	0.76	3.1E-01	Z74883.1	NT	S cerevisiae chromosome XV reading frame ORF YOL141w
5729	18922		0.83	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6595	19755	33141	1.3	3.1E-01	AW983548.1	EST_HUMAN	RC3-HN0001-310300-011-bp4 HN0001 Homo sapiens cDNA
6683	19822	33209	0.96	3.1E-01	AI264458.1	EST_HUMAN	ql39401.x1 NCI_CGAP_Co6 Homo sapiens cDNA clone IMAGE:1874689 3'
6821	19974	33382	0.79	3.1E-01	X71887.1	NT	H sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6905	20220		0.69	3.1E-01	AW377354.1	EST_HUMAN	MF32-G10222-281099-005-h05 C10222 Homo sapiens cDNA
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	601308121 F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7856	20911	34416	0.7	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	Yd48701.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
10106	23144	36742	0.68	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10272	23307	36903	1.04	3.1E-01	BF696339.1	EST_HUMAN	602124743 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36904	1.04	3.1E-01	BF696339.1	EST_HUMAN	602124743 F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10334	23369	36979	1.68	3.1E-01	A1244001.1	EST_HUMAN	q181e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S56700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10510	23545		0.98	3.1E-01	T55525.1	EST_HUMAN	y647h08.s1 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	601883592 F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24833	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xa02g09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24816	38507	2.08	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24817	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	y989b05.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element;
12123	25103		1.3	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25286		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304182.1	NT	Silvestrodon vitreum 40S ribosomal protein S11 mRNA, partial cds
12613	25412		3.73	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26877		3.82	3.1E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
13088	26123		1.22	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp1-pending), mRNA
74	15979	26336	1.85	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xs6308.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1537	14690	27769	5.77	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
1838	14984	28084	1.2	3.0E-01	X69082.1	NT	A. imnerus putative gene encoding integrase, Mars2 (RP)
3069	16245		0.8	3.0E-01	AB008677.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	16457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 algPG gene for polyglucuronate lyase, complete cds
3988	17123	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281199-001-g01 ST0262 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5258	19949	28665	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5467	18667	31646	5.1	3.0E-01	BE741628.1	EST_HUMAN	601594960.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18746	31780	0.64	3.0E-01	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBED2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
5621	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5621	18815	31884	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5658	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6970	20198	33624	2.82	3.0E-01	D16313.1	NT	Mouse cyclophilin 18 gene, complete cds
6889	18518	31511	0.76	3.0E-01	U02389.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7095	20118	33532	1.15	3.0E-01	AF229247.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33806	0.98	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20569	34028	4.3	3.0E-01	10847007	NT	Mus musculus midnolin (Midn-pending), mRNA
7670	20738	34214	1.61	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBLS PspA (pspA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8598	21649		3.1	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9e), mRNA
8658	21738	35279	0.48	3.0E-01	Z70200.1	NT	H. sapiens gene for US enRNP-specific 200kD protein
8671	21751	35288	1.23	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8029	22108	35649	0.69	3.0E-01	AF141876.1	NT	Streptomyces sulfonolactis isopenicillin N synthase (pcbC) gene, partial cds
9072	22151		0.82	3.0E-01	7681685	NT	Homo sapiens DKFZP568M0122 protein (DKFZP568M0122), mRNA
9419	22493	36059	1.09	3.0E-01	AF220507.1	NT	Anabaena POC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOTHEICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9927	22967		0.48	3.0E-01	D90904.1	NT	Synedococcus sp. PCC8803 complete genome, 6127, 630555-781448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10346	23381	36992	0.45	3.0E-01	AF152598.3	NT	Acetobacillus actinomycetomorphans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10346	23381	36993	0.46	3.0E-01	AF152598.3	NT	Acetobacillus actinomycetomorphans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10608	23640	37248	0.8	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BIP, complete cds
10629	23683	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10629	23683	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12067	25048	38755	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048	38756	2.16	3.0E-01	H51028.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.49	3.0E-01	AJ297631.1	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ249895.1	NT	Mus musculus mae proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1830	15073	26176	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2322	16454	28585	1.01	2.9E-01	AF222718.1	NT	Chrysididymus synuloides mitochondrion, complete genome
3253	16427	28445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2f mRNA, complete cds

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3323	16496	29513	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3323	16496	29514	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
4003	17160	30166	1.12	2.9E-01	AI610836.1	EST_HUMAN	tp21a1.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb-D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	wf14d10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F6.7 CE15576;
4183	17333	30325	0.61	2.9E-01	AB016428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4195	17345		0.79	2.9E-01	AW002902.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
4608	17745	30724	0.98	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4957	18087	31063	0.59	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.99	2.9E-01	AI670899.1	EST_HUMAN	wr09f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287308 3' similar to contains L1.L2 L1 repetitive element;
5320	18087	31063	0.65	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18576		1.59	2.9E-01	R37485.1	EST_HUMAN	y77e12.x1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suadeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P28, P30 and levanase
5884	19073	32382	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P28, P30 and levanase
5897	19085	32397	5.53	2.9E-01	6679662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
6181	19357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	z97b12.1 Soares NIHMPu ST Homo sapiens cDNA clone IMAGE:767711 5'
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	wr27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.L1 L1 repetitive element;
6455	19622	32986	2.22	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suadeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7126	18552	31466	1.4	2.9E-01	AF142329.1	NT	Mus musculus Filh protein (Filh) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Brlg1 (BING1), tapasin (tapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1, 3-galactosyl tr>
7310	20352	33852	1.54	2.9E-01	AF100958.1	NT	60106830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	801065630F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8358	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	601882670F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
							Buchnera aphidicola plasmid pL eu isolate M1 2-isopropylmalate synthase (lucA) gene, partial cds; 3-isopropylmalate dehydrogenase (lucB) gene, complete cds; and isopropylmalate dehydratase subunit (lucC) gene, partial cds
8834	21615		0.53	2.9E-01	AF167456.1	NT	
8794	21873	35412	0.82	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9125	22204	35747	1.09	2.9E-01	AF226908.1	NT	Arabidopsis thaliana sulfonurea receptor-like protein mRNA, complete cds
9233	22311	35863	0.81	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1-H-B12-shg-b-02-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	U1-H-B12-shg-b-02-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
11133	24206	37830	1.94	2.9E-01	AF128843.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38159	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
							ny35h02.e1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
11881	24869	38566	2.71	2.9E-01	AA93373.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
11886	24874	38571	3.12	2.9E-01	AL139078.2	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							w28505.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER28 repetitive element;
12877	25452	32017	1.85	2.9E-01	AW005671.1	EST_HUMAN	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene I
12774	25516		1.89	2.9E-01	V00202.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12777	25519	32001	2.23	2.9E-01	AF082453.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13126	25734	31944	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13126	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31919	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein. CdMT-1 mRNA, complete cds
582	13774		2.04	2.9E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
587	13778		1.95	2.9E-01	L28145.1	NT	Ptarmica dwarf virus movement protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds
1306	14462	27529	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1308	14462	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW89020.1	EST_HUMAN	QV1-CT0384-120200-085-b05 CT0384 Homo sapiens cDNA
2089	15210	28326	1.49	2.8E-01	AL047620.1	EST_HUMAN	DKFZp386l2321_1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp386l2321
2200	16335	28462	1.51	2.8E-01	AW511185.1	EST_HUMAN	hd44603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2542	15657	28791	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2642	15657	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	16948	28958	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	29234	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3038	16212	29235	2.62	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3466	16633	29652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt, position (4/7)
4103	17257	30257	1.87	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 88 of 70) of the complete genome
4240	17388		0.6	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_Jestis_NHT Homo sapiens cDNA clone IMAGE:1040228 3' similar to contains Alu repetitive element; contains element MCR22 repetitive element ;
4592	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF076238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31090	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4180129 5'
5006	18135	31109	3.66	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element ;
5318	18473	31404	0.61	2.8E-01	X60787.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5428	25804	31602	23.61	2.8E-01	AA349897.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5723	18918	32211	2.57	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW892583.1	EST_HUMAN	GM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765266.1	EST_HUMAN	cao1006.61 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:U34539 FK508-BINDING PROTEIN (HUMAN);
6059	19241		0.64	2.8E-01	AA404576.1	EST_HUMAN	ZK4101.1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	26212		0.87	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6347	19517	32874	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511216.1	EST_HUMAN	UI-H-B14-eel-F04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthomyx heterodius cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20599		1.14	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1, 5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8284	21366	34885	1.31	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	qp48h01.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
						NT	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
						NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	35328	0.6	2.8E-01	AA911629.1	EST_HUMAN	c02h05.s1 NCI CGAP C012 Homo sapiens cDNA clone IMAGE:1419693 3' similar to gb:M87789 IG
8789	21888		7.72	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
9666	22628	36109	1.14	2.8E-01	U17251.1	NT	802022987F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4186525 5'
9612	22952		1.16	2.8E-01	L13654.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23193	36789	0.7	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10265	23300	36898	3.8	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10519	23534		1.1	2.8E-01	9628164	NT	Fujikami sarcoma virus, complete genome
10561	23595	37202	0.5	2.8E-01	BE959727.2	EST_HUMAN	801654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10982	24081	37695	1.88	2.8E-01	BF241062.1	EST_HUMAN	801880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10982	24081	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	801880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24090	37727	3.01	2.8E-01	BF695970.1	EST_HUMAN	801852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11119	24191	37823		2.8E-01	AF051862.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11556	24611		3.58	2.8E-01	BF674023.1	EST_HUMAN	802137418F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4273853 5'
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
11851	24840	38534	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D63329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25562	31987	7.61	2.8E-01	BE178999.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12875	25592	31996	1.29	2.8E-01	BE900116.1	EST_HUMAN	801673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955096 5'
13052	26068		1.59	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
489	13683	26717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus GSK104 mRNA
628	13613	26835	13.64	2.7E-01	AA450061.1	EST_HUMAN	xx39b10 s1 Soares_tetral_virus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains <i>Alu</i> repetitive element;
1200	14446	27512	2.04	2.7E-01	AB004908.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01	X78815.1	NT	G.lambia SR2 gene
1768	14917	28012	3.16	2.7E-01	W58067.1	EST_HUMAN	zid2h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14968	28059	1.46	2.7E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular merozoite transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	A1372772.1	EST_HUMAN	EST175678 Infant brain, Bonto Soares Homo sapiens cDNA clone UH1801R 5' end
2250	15383	28511	0.94	2.7E-01	A1372772.1	EST_HUMAN	EST175678 Infant brain, Bonto Soares Homo sapiens cDNA clone UH1801R 5' end
2440	15568	28695	7.07	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (H88), partial
2526	15651	28775	4.36	2.7E-01	A1310858.1	EST_HUMAN	ta43d11.x2 NCL CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3048	16225		0.99	2.7E-01	BF088284.1	EST_HUMAN	CM1-PT0875-060600-385-e03 HT0875 Homo sapiens cDNA
3381	16533	29547	0.66	2.7E-01	8393620	NT	Rattus norvegicus Insulin receptor (<i>Insr</i>), mRNA
4118	17272	30271	1.94	2.7E-01	A1928016.1	EST_HUMAN	wo52et11.x1 NCL CGAP_Xid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17296	30281	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (<i>ae6</i>) gene, partial cds
4133	17286	30282	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (<i>ae6</i>) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77569.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
5153	18275		4.48	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5381	18583	31452	1.98	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA4 (CHOX-1.4)
5507	18802		1.31	2.7E-01	AB033171.1	NT	Astropora myriophthalma mitochondrial cytb gene for cytochrome b, partial cds
6472	19639	32998	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6472	19639	32999	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6745	19801	33293	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6745	19801	33294	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6918	20233	33697	1.74	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7197	20082		0.77	2.7E-01	A1640070.1	EST_HUMAN	td08f08.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7511	20585	34098	0.92	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7865	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7865	20919	34428	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20988	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7917	20988	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7976	21026	34540	0.66	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.66	2.7E-01	AA013147.1	EST_HUMAN	z35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
8330	21412	34938	0.56	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0062-100500-002-409 SN0062 Homo sapiens cDNA
8380	21461	34934	0.66	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8466	21567	35104	0.83	2.7E-01	AL181552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35690	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VOLT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9534	22599	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9537	22602		2.86	2.7E-01	P37928	SWISSPROT	FIMBRIN W PROTEIN
10005	23043	36636	0.8	2.7E-01	D89680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10323	23358	36868	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23782		0.51	2.7E-01	AB011679.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCC005 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCC005 5'
11061	24137	37772					Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12816	25942		2.58	2.7E-01	AJ133259.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
13034	25881		1.49	2.7E-01	AB008782.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 6
482	16013	26710	2.75	2.7E-01	AF217491.1	NT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX2
			2.8	2.6E-01	P78411	SWISSPROT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
483	13688		1.94	2.6E-01	D19459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1488	14822	27705	1.08	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1945	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							b604d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2169	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	M11844.1	NT	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
2611	16735		11.68	2.6E-01	BE272440.1	EST_HUMAN	EST386635 IMAGE resequences, MAGF Homo sapiens cDNA
3161	16836		1.11	2.6E-01	AW874531.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3671	16834	29845	0.84	2.6E-01	M22342.1	NT	
3733	16894	29899	1.67	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
4215	17364	30352	0.79	2.6E-01	AW659510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4476	17616	30597	1.71	2.6E-01	AF175283.1	NT	Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4617	17754	30735	0.89	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30736	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4870	17805	30704	1.14	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stratiocarpus foetalis retinal g37202 Homo sapiens cDNA clone IMAGE:638477 5'
4770	17905	30897	2.26	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type II chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	y51605.11 Soares placenta Nb214F Homo sapiens cDNA clone IMAGE:152288 5'
5195	18277		0.61	2.6E-01	AA884825.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488605 3'
5457	18657		1.29	2.6E-01	AB035872.1	NT	Paramacium caudatum gene for PAP, complete cds
5565	18762	31802	0.67	2.6E-01	M98060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5680	18883		0.84	2.6E-01	A862398.1	EST_HUMAN	tdt16a03.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element
							Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor TGHM enhancer 3 genes, partial cds; and unknown g>
5895	19053	32394	0.64	2.6E-01	AF207550.1	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6166	26211		2.57	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6330	19501	32859	1.96	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6330	19501	32860	1.96	2.6E-01	AI582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT
6552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8807	19961	33364	0.74	2.6E-01	BE792052.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8807	19961	33365	0.74	2.6E-01	BE792052.1	EST_HUMAN	801581764F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	801581764F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7549	20621	34098	0.7	2.6E-01	BE148961.1	EST_HUMAN	801581764F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7587	25843		0.96	2.6E-01	AL139077.2	NT	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7626	20693		0.78	2.6E-01	AA196149.1	EST_HUMAN	CMC-HT0245-031199-085-f04 HT0245 Homo sapiens cDNA
7918	20969	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	z092e01.r1 StrataGene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	y07a03.g1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8529	21610	35148	2.97	2.6E-01	BF343588.1	EST_HUMAN	y082a07.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124212 5'
8605	21696	35223	1.74	2.6E-01	Q10199	SWISSPROT	MRO-HT0166-181199-003-412 HT0166 Homo sapiens cDNA
8892	21971	35506	4.06	2.6E-01	BE830339.1	EST_HUMAN	602014422F1 NCI_CGAP_Br64 Homo sapiens cDNA clone IMAGE:4150396 5'
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	HYPOHETICAL 75.2 KD PROTEIN G11G11.02 IN CHROMOSOME II
9667	22629	36200	0.92	2.6E-01	X17804.1	NT	RC8-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22629	36200	0.92	2.6E-01	X17804.1	NT	RC8-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22629	36200	0.92	2.6E-01	X17804.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9667	22629	36200	0.92	2.6E-01	X17804.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9940	22979		0.5	2.6E-01	AF057121.1	NT	cds
10072	23110	36713	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10072	23110	36714	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10393	23428		0.63	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11815	24804		31.14	2.6E-01	X51755.1	NT	Human lambdaB-immunoglobulin constant region complex (germline)
12468	28070		4.14	2.6E-01	BE830491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	25365	32069	3.85	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (PXYD2) gene, complete cds, alternatively spliced

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
13007	25603		1.78	2.6E-01	AE001713.1	NT	Thermodoga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.6E-01	AF141925.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13098	15735		1.43	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960043 5'
13107	25722		2.04	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.6E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	28503	1.87	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
282	13472	28503	1.7	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
285	13484		2.51	2.5E-01	IM28501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U09964.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1055	14251		1.75	2.5E-01	AE002158.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1787	14916		4.53	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15608		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2593	15698	28814	1.22	2.6E-01	6579216	NT	Mus musculus protein-L-isospartate (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2595	15890		1.02	2.5E-01	AA251987.1	EST_HUMAN	2s11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2702	15920	28838	1	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3488	16555		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3639	16803	29816	7.18	2.6E-01	AL161617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3950	17108	30105	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4436	17578		0.88	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-18
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30893	3.99	2.5E-01	AF007768.1	NT	Charistinaura fumiferana diaphase associated protein 2 (DAP2) mRNA, complete cds
4904	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4926	18056		3.54	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31080	0.8	2.5E-01	BE889785.1	EST_HUMAN	601437488F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4994	18123	31101	0.61	2.5E-01	U83656.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	z65a05.1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755600 5' similar to gb:M88279
5441	18641	31620	12.21	2.5E-01	S83390.1	NT	P59 PROTEIN (HUMAN);
6080	19282	32591	0.6	2.5E-01	AJ006345.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6081	19293		0.81	2.5E-01	AL163207.2	NT	Homo sapiens KVLQT1 gene
6762	19918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C007
7190	20055	33485	0.64	2.5E-01	8394138	NT	Homo sapiens partial steerin-1 gene
7507	20581	34054	0.71	2.5E-01	U13992.1	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7536	20609		1.13	2.5E-01	AF134119.1	NT	Feline calicivirus CF/108 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7770	20828	34319	0.62	2.5E-01	AL161608.2	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7814	20869	34365	4.23	2.5E-01	AL163282.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8028	21111	34630	2.22	2.5E-01	BF109040.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
8039	21122	34642	0.61	2.5E-01	BE980712.1	EST_HUMAN	757a03.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8421	21502	35034	1.9	2.5E-01	BF086595.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	601459238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'
8837	21916	35454	4.07	2.5E-01	H53236.1	EST_HUMAN	ETB PROTEIN, SMALL T-ANTIGEN (ETB 19K)
9076	22155	35609	1.05	2.5E-01	M88826.1	NT	y8407.11 Scores fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:202501 5'
9716	22781	36351	10.85	2.5E-01	U89651.2	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9772	22788	36339	2.44	2.5E-01	AF085164.1	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22788	36340	2.44	2.5E-01	AF085164.1	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
10303	23338	36943	1.31	2.5E-01	AW881997.1	EST_HUMAN	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10550	23695	37193	0.51	2.5E-01	11465632	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10763	23793	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	RC3-ST0186-130100-015-a07 S70186 Homo sapiens cDNA
10787	23800	37422	1.61	2.5E-01	X58491.1	NT	Pocphyra purpurea chloroplast, complete genome
11332	24395	38043	2.96	2.5E-01	D50914.1	NT	xg40c10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
12204	25198	38834	5.16	2.5E-01	AF200528.1	NT	Mouse L1Md LINE DNA
12233	26167		6.12	2.5E-01	AL191641.2	NT	Human mRNA for KIAA0124 gene, partial cds
						NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	26674		1.22	2.5E-01	AF325963.1	NT	Delta brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA096316.1	EST_HUMAN	on70d04.g1 Sceres_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	902132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271678 6'
1332	14489	27557	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1332	14499	27568	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1415	14596	27642	0.97	2.4E-01	Y12983.1	NT	Homo sapiens FLI-1 gene, partial
1888	16041		26.78	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1940	15092	28193	1.43	2.4E-01	AF251708.1	NT	Zaocys dhumades fructose-1,6-bisphosphatase mRNA, complete cds
2091	15231	28353	1.64	2.4E-01	A1742958.1	EST_HUMAN	TR:O60287 O60287 KIAA0512 PROTEIN ;
2206	15340	28487	1.17	2.4E-01	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT PROTEASE)
2336	15487	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D. discoideum (Ax3-K) ponA gene
2820	15934	29046	2.22	2.4E-01	X71783.1	NT	S. pombe ewf6 gene
2848	15930	28069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3217	16381	29402	1.51	2.4E-01	X74209.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3856	17016	30018	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17283		0.65	2.4E-01	D28980.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31266	0.65	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31267	0.65	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5334	18447	31415	1.89	2.4E-01	U88914.1	NT	Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfurtransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa
5335	18448	31416	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU1281-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU1281-TY, exon 13
5578	18773	31818	0.9	2.4E-01	A1825707.1	EST_HUMAN	wc33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5578	18773	31819	0.9	2.4E-01	A1825707.1	EST_HUMAN	wc33d05.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5602	18787	31947	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18964	32266	12.86	2.4E-01	AF091218.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5772	18964	32267	12.86	2.4E-01	AF091218.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5800	18950		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	25815		0.97	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calm2 gene)
							716404.x1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
							Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6016	19200	32517	2.54	2.4E-01	BF592336.1	EST_HUMAN	
6108	19288	32820	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6215	19390	32738	2.49	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6269	19443	32792	0.94	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cdA Homo sapiens cDNA clone cdAADE11 5'
6616	19881	33051	0.87	2.4E-01	AA39872.1	EST_HUMAN	z70d02.s1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:727683 3'
							w62c11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
							PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
6665	19824	33212	1.59	2.4E-01	A1698989.1	EST_HUMAN	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7498	20673	34046	7.79	2.4E-01	L43001.1	NT	Mus musculus DX1mx48a protein (DX1mx48a) mRNA, complete cds
7902	20954	34481	0.68	2.4E-01	AF223644.1	NT	Mmusculus pah gene and promotor
8271	21353	34968	0.5	2.4E-01	X97252.1	NT	Mmusculus pah gene and promotor
8271	21353	34969	0.5	2.4E-01	X97252.1	NT	Mmusculus pah gene and promotor
8392	21473	34999	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h008 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h008 genes; two component system 08
8544	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8798	21877	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106288 5'
9332	22408	35951	0.39	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9332	22408	35962	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
							wd43602.x1 Scores, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330606 3' similar to contains
9763	22701	36287	8.39	2.4E-01	A1693515.1	EST_HUMAN	MER22.b1 TAR1 repetitive element;
9905	22945	36530	0.69	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22945	36531	0.66	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10654	23689	37297	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11006	24085	37722	2.15	2.4E-01	AL181494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24149	37786	1.96	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24508	38174	1.8	2.4E-01	BE296917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE296917.1	EST_HUMAN	601176416F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537		8.04	2.4E-01	Z21647.1	NT	P. asiatica mosaic virus genomic RNA
12169	25127	39827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12288	25932		1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12360	25258		1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12988	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12839	26151		1.37	2.4E-01	BF228975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13072	26701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BRK gene)
13102	25718		4.16	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13597	26633	1.39	2.3E-01	S75889.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]
854	13840		5.53	2.3E-01	U98713.1	NT	Mycoplasma genitalium section 33 of 51 of the complete genome
884	13969	26900	29.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 160 of the complete genome
957	14130	27188	3.57	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1834	14786	27872	1.11	2.3E-01	AJ245480.1	NT	Braconia napsus sig gene for S-locus glycoprotein, cultivar T2
1861	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdi5 gene, exon 1, partial
2103	15242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2517	15643	28764	1.85	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2717	15633	28945	0.88	2.3E-01	M11318.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB019033.1	NT	Martellia agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain JFO 14957
3028	16204	29227	1.08	2.3E-01	AA801378.1	EST_HUMAN	nc16d06.s1 NCL_OGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	repetitive element; contains element THR repetitive element ;
3456	16623	28644	1.32	2.3E-01	H68836.1	EST_HUMAN	Yn21507.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
							Yn9710.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
							GSTA5=glutathione S-transferase Yc2 subunit [5' region, intron 1] [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3944	17103	30100	0.98	2.3E-01	S82821.1	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4046	17202		5.15	2.3E-01	7662133	NT	Y17701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4470	17810	30588	0.86	2.3E-01	R82252.1	EST_HUMAN	Mus musculus retin (Ret-1c) gene, promoter region
4520	17659		1.91	2.3E-01	L78789.1	NT	Synecocystis sp. PCC6803 complete genome, 1/27, 1-133859
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4611	17748	30728	2.76	2.3E-01	AF092535.1	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4876	17811	30800	5.65	2.3E-01	5031984	NT	Mus musculus tulip 1 mRNA, complete cds
5159	18281	31246	0.87	2.3E-01	AB032400.1	NT	
							Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5223	18345		1.03	2.3E-01	M19364.1	NT	602192210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5280	18379	31345	0.63	2.3E-01	BF374804.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
5419	18520	31596	2.47	2.3E-01	AB040945.1	NT	7k30606.x1 NCL_OGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476659 3' similar to SW-GAG_SMSAV
							P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;
5645	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5647	18841	32122	5.25	2.3E-01	X86587.1	NT	C.familiaris rom1 gene
5766	18958		0.99	2.3E-01	L39112.1	NT	Vitiforma corneum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Leuostoeus canosum, Genomic, 2866 nt]
6062	19244	32559	1.98	2.3E-01	A1708840.1	EST_HUMAN	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6062	19244	32570	1.98	2.3E-01	A1708840.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6794	19949	33348	0.66	2.3E-01	AF198089.1	NT	as27612.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7017	20153	33573	4.63	2.3E-01	A1718148.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7260	20343	33796	0.86	2.3E-01	8923323	NT	Oxytolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	as42712.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element
7573	20645	34123	2.34	2.3E-01	AF173369.1	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7576	20648	34125	5.37	2.3E-01	AV719681.1	EST_HUMAN	Secale cereale omega secalin gene, complete cds
7576	20648	34126	5.37	2.3E-01	AV719681.1	EST_HUMAN	Glycine max resistance protein LM17 precursor RNA, partial cds
7784	20840		4.26	2.3E-01	8754779	NT	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7789	20845	34338	1.56	2.3E-01	BE888071.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLCDB08 5'
7831	20881		2.8	2.3E-01	NB0983.1	EST_HUMAN	Mus musculus myosin XV (Myo15), mRNA
7968	21018	34530	0.71	2.3E-01	11416821	NT	601311573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7968	21018	34531	0.71	2.3E-01	11416821	NT	zr12e08.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:292358 5'
8035	21118	34637	0.52	2.3E-01	AL161558.2	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
8183	21265	34788	1.73	2.3E-01	M68931.1	NT	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
8690	21770	35300	0.82	2.3E-01	U57989.1	NT	Arabidopsis thaliana DNA chitosome 4, contig fragment No. 58
8972	22051	35594	0.58	2.3E-01	AW090541.1	EST_HUMAN	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
9089	22168	35715	0.52	2.3E-01	AW090541.1	EST_HUMAN	Mus musculus prosaposin (psap)(SGP-1) gene, complete cds
9341	22417	35970	0.84	2.3E-01	AA372184.1	EST_HUMAN	xs90e06.x1 NCL CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2591554 3'
9341	22417	35971	0.64	2.3E-01	AA372184.1	EST_HUMAN	EST376533 MAGC resequences, MAGH Homo sapiens cDNA
9760	22820	36398	0.53	2.3E-01	BE277890.1	EST_HUMAN	EST376533 MAGC resequences, MAGH Homo sapiens cDNA
9830	22870	36559	0.53	2.3E-01	BE277890.1	EST_HUMAN	EST376533 MAGC resequences, MAGH Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63338)
9885	23024	36616	0.81	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGC resequences, MAGH Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63338)
10037	23075	36675	1.57	2.3E-01	X52124.1	NT	EST376533 MAGC resequences, MAGH Homo sapiens cDNA
							Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10071	23109	36712	0.83	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281289-001-104 DT0036 Homo sapiens cDNA
10138	23176	36773	2.62	2.3E-01	BE173080.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	36823	2.48	2.3E-01	AJ263281.1	NT	Rhizabium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10671	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4102082 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11833	24713	38404	2.43	2.3E-01	AE002187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12088	25079		1.36	2.3E-01	AV709738.1	EST_HUMAN	AV709738 ADC Homo sapiens cDNA clone ADCAGH01 5'
12281	25210		3.07	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25284		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
12395	25873		1.23	2.3E-01	AA089819.1	EST_HUMAN	chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12484	26088	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q8Z175
12500	28143	31552	7.05	2.3E-01	BE882484.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element;
12553	25378		1.77	2.3E-01	BF663319.1	EST_HUMAN	60150720F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908699 5'
12612	25411		2.74	2.3E-01	AJ006519.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12708	25470		1.22	2.3E-01	U49845.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	25411		1.84	2.3E-01	AJ006519.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
13009	25665		2.36	2.3E-01	BF475611.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13327	26355	1.13	2.2E-01	A1052190.1	EST_HUMAN	nc39h12.x1 Lupeki_solito_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
1598	14749	27833	2.74	2.2E-01	AF187850.1	EST_HUMAN	MER39 repetitive element;
2155	15291	28418	2.19	2.2E-01	M34640.1	NT	0274610.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to
2478	15803	28726	7.16	2.2E-01	BF677538.1	EST_HUMAN	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2654	15777	28890	1.63	2.2E-01	BE618258.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2654	15777	28891	1.63	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2946	16123	28136	4.94	2.2E-01	BE155625.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249869 5'
2946	16123	28137	4.94	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	28137	4.94	2.2E-01	BE155625.1	EST_HUMAN	601462629F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	28137	4.94	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
2946	16123	28137	4.94	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
2987	16163		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3479	16646		2.35	2.2E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3848	17008	30009	0.82	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17380	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.6	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	6.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4379	17522	30503	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.08	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31059	2.2	2.2E-01	AA211216.1	EST_HUMAN	2887c05.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE147035.1	EST_HUMAN	MRQ-H70067-201089-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.88	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DAPH2), transcript variant 156, mRNA
5874	19084		3.75	2.2E-01	D84000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6122	19301	32640	0.78	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6845	19998	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7166	20299	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7279	20362	33815	1.81	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7279	20362	33816	1.81	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7442	20519	33991	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7655	20723	34199	0.82	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7878	20930	34436	0.68	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7905	20957	34463	0.71	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8210	21292		2.45	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8280	21362	34881	2.68	2.2E-01	Z48933.1	NT	E.coli sepA and sepB genes
8748	21827	35363	0.61	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9097	22176	35720	4.59	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9117	22188	35740	0.48	2.2E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cdo
9224	22302		2.88	2.2E-01	AW855036.1	EST_HUMAN	PM3-CT0263-241298-008-507 CT0263 Homo sapiens cDNA
9316	22381	35942	1.98	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9489	22546	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	z0408.t1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:291591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22817	36187	0.78	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (klp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9576	22718	36206	4.29	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9820	22860	36441	0.65	2.2E-01	Q60980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23088	36854	3.84	2.2E-01	AF187941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (OPeHSP21) mRNA, complete cds; nuclear gene for chloroplast product
10159	23196	36782	1.53	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10380	23416	37024	1.11	2.2E-01	9626671	NT	Human herpesvirus 5, complete genome
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	y633d08.t1 Stralagene ovary (H937217) Homo sapiens cDNA clone IMAGE:75855 5'
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y633d08.t1 Stralagene ovary (H937217) Homo sapiens cDNA clone IMAGE:75855 5'
							Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinol quinone synthesis A (pqoA) genes, complete cds; and pyrroloquinol>
10580	23616	37220	0.6	2.2E-01	AF089264.1	NT	Mus musculus PHR1 (Phr1) gene, partial cde
10659	23693		0.79	2.2E-01	AF071001.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37345	0.67	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	23868	37605	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and A5
11389	24450	38111	1.65	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24704	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11748	23934	37560	3.7	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51560), mRNA
12207	25161		1.33	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12319	26156		1.96	2.2E-01	U82871.2	NT	

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	26286		3.24	2.2E-01	AF198843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.86	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141198-021-g04 CT0249 Homo sapiens cDNA
12519	26353		1.47	2.2E-01	AW961922.1	EST_HUMAN	h17502.X1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
13115	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKCC Homo sapiens cDNA clone GKCAHB02 5'
893	14165	27226	1.88	2.1E-01	AA566289.1	EST_HUMAN	hm31611.s1 NCI_CGAP_L1p2 Homo sapiens cDNA clone IMAGE:1061804
998	14187	27228	0.72	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27446	1.45	2.1E-01	6754239	NT	Mus musculus interferon (alpha and beta) receptor 2 (fnar2), mRNA
1225	14385	27447	1.45	2.1E-01	6754239	NT	Mus musculus interferon (alpha and beta) receptor 2 (fnar2), mRNA
1540	14692	27771	4.29	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1963	15106	28206	2.15	2.1E-01	AA906824.1	EST_HUMAN	6k73e02.s1 NCI_CGAP_GG4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2224	16358	28488	3.55	2.1E-01	BF693073.1	EST_HUMAN	COMPLEMENT C3-PRCUCRSOR (HUMAN); 602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2991	16167	29183	2.52	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3533	16698	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	nc90b10.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1159579 3'
3908	17067		5.81	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
4125	17279		0.87	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4165	17315	30310	1.57	2.1E-01	P11075	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4165	17315	30311	1.57	2.1E-01	P11075	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4495	17635		1.63	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens pschp47 gene, complete cds
4767	17892	30871	0.93	2.1E-01	X93161.1	NT	P.falcipterus mRNA for small GTPase rab11
5138	18261	31228	0.7	2.1E-01	D13587.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5416	18618	31592	6.31	2.1E-01	BF672895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
7027	20163	33585	1.05	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial
7038	20091	33508	1.8	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7584	20936	34111	0.77	2.1E-01	Q01998	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7584	20936	34112	0.77	2.1E-01	Q01996	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7576	20847		1.89	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7883	20835	34441	1.54	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
7930	20980	34488	1.38	2.1E-01	AF066887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7930	20680	34489	1.38	2.1E-01	AF088687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
8700	21780	35313	4.79	2.1E-01	U88399.1	NT	Haemophilus influenzae hmcD, putative haemochromin processing protein (hmcC), putative ABC transporter (hmcB), putative haemochromin structural protein (hmcA), and haemochromin immunity protein (hmcI) genes, complete cds
8897	22076	35615	0.81	2.1E-01	AL040597.1	EST_HUMAN	DKFZp434H0614.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5
8997	22076	35616	0.91	2.1E-01	AL040597.1	EST_HUMAN	DKFZp434H0614.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614.5
9159	22237		0.5	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
9237	22314	35856	6.7	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025W
9704	22753	36323	0.66	2.1E-01	N42538.1	EST_HUMAN	Y11e10.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270954.5
9704	22753	36324	0.66	2.1E-01	N42538.1	EST_HUMAN	Y11e10.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270954.5
9713	22776	36349	2.72	2.1E-01	X97378.1	NT	A.thaliana mRNA for AFRanBP 1b protein
9817	22857	36437	1.02	2.1E-01	AB036528.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10535	23570	37178	1.31	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10569	23604	37209	1.97	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10578	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE
11776	24768		1.34	2.1E-01	A1141575.1	EST_HUMAN	802131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831.5
11862	24850		1.68	2.1E-01	11038647	NT	qac6108.x1 Soares fetal heart_Nb-H19W Homo sapiens cDNA clone IMAGE:1661751.3
11879	24867	36565	2.6	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
12688	25459		1.92	2.1E-01	AF217490.1	EST_HUMAN	RC3-H1T0622-040500-013-b11 H1T0622 Homo sapiens cDNA
12994	25646		1.39	2.1E-01	BE622149.1	EST_HUMAN	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
13158	25753	31928	1.79	2.1E-01	AJ276505.1	NT	801440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675.5
205	13428	26460	1.92	2.0E-01	AB017437.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
547	13740		1.97	2.0E-01	7705601	NT	Gallus gallus mRNA for avian, complete cds
717	13899	26937	1.37	2.0E-01	IM77085.1	NT	Homo sapiens CGI-18 protein (LOC51009), mRNA
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	O. cuniculus germine IgH heavy chain V-H pseudogene, allotype VH2
1036	14204	27261	1.83	2.0E-01	D8905.1	NT	Mus musculus Major Histocompatibility Locus class II region
1149	14313	27368	2.81	2.0E-01	AL163213.2	NT	Synedocystis sp. PGC8803 complete genome, 7/27, 781446-820615
1283	14439	27508	1.19	2.0E-01	AJ132995.6	NT	Homo sapiens chromosome 21 segment HS21C013
1336	14493	27563	1.99	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1516	14689	27752	22.4	2.0E-01	4603408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1562	14734	27816	2.68	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.96	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1785	14904		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1796	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2955	16132		0.79	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH88A11
3576	16741	29758	0.72	2.0E-01	P46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.91	2.0E-01	AW238005.1	EST_HUMAN	xp1502.x1 NCL CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3798	16959	29963	0.86	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3802	16963		0.6	2.0E-01	6680797	NT	CED-11 PROTEIN
4688	17823		8.71	2.0E-01	BE828165.1	EST_HUMAN	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
5152	18274	31243	6.41	2.0E-01	8922080	NT	QV4-EN0032-180500-223-e03 EN0032 Homo sapiens cDNA
5243	18959	29963	0.8	2.0E-01	P34641	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5581	18758	31797	2.55	2.0E-01	X86600.1	NT	CED-11 PROTEIN
5859	19049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5963	19149	32464	0.82	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valy-rRNA synthetase
6303	19476		0.74	2.0E-01	M75987.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
6659	19818	33208	3.74	2.0E-01	AW360866.1	EST_HUMAN	Mauritius mu class glutathione transferase gene
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141098-001-g06 CT0247 Homo sapiens cDNA
7603	20573	34147	0.83	2.0E-01	P64422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (Pfkfb) gene, exons 3 through 7
8139	21221		6.16	2.0E-01	AF028028.1	NT	GAVMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21478	35003	3.12	2.0E-01	X91151.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
8921	22000		0.48	2.0E-01	BE562247.1	EST_HUMAN	M. musculus scp2 gene exon 14
9551	22618	36188	1.17	2.0E-01	U82511.1	NT	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9590	22845	36215	0.62	2.0E-01	U71122.1	NT	Dicystotellium discoidium random slug cDNA19 protein (rsc19) mRNA, partial cds
9756	22694		5.42	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9847	22986	36579	0.52	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
9847	22986	36580	0.52	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10095	23133		2.24	2.0E-01	AF146692.1	NT	DAUGHTERLESS PROTEIN
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23408	37016	0.87	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23408	37017	0.87	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23454		0.8	2.0E-01	X78388.1	NT	D melanogaster DNA mobile element (hoppe)
10616	23650	37259	0.88	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
11078	24154	37791	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11078	24154	37792	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38597	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
11908	24895	38598	1.33	2.0E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	AF206837.2	NT	Pinophytes promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12899	25985		1.64	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Ltn isoform (ninein) mRNA, complete cds
12912	25976	31851	1.63	2.0E-01	AW975297.1	EST_HUMAN	EST1387405 MAGC resequences, MAGN Homo sapiens cDNA
12962	25662	31966	1.63	2.0E-01	AI023592.1	EST_HUMAN	on08a10.31 Soares testis NHT Homo sapiens cDNA clone IMAGE:1843810 3'
12977	25636		17.48	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
113	13344		4.89	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
382	13573	26604	5.58	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13859	26889	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambricola protein kinase C-interacting protein mRNA, complete cds
673	13859	26890	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambricola protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
681	13866	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1070	14181		1.72	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (il2rg), mRNA
1128	14283	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST07784 Fetal lung II Homo sapiens cDNA 5' and
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa lefflin cluster
1466	14820		4.34	1.9E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2456	15584	28711	3.66	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2989	16165	29181	3.81	1.9E-01	U68066.1	NT	Sigmodon hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16850	29668	4.07	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3569	16734	29750	4.94	1.9E-01	R16467.1	EST_HUMAN	Y42710.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129547 5'
3907	17068	30065	1.09	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4100	17255	30256	3.68	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4183	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	GM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4231	17397		1.31	1.9E-01	AE001812.1	NT	Deinococcus radiodurans R1 section 48 of 229 of the complete chromosome 1

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489	30471	0.89	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4592	17729	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18250		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	x28a07.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2618444 3' similar to gb:M73779 RETINOIC
5761	18953	32256	8.03	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
5952	19148	32463	1.08	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6006	19191		2.45	1.9E-01	AU133116.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
6457	19824	32987	1.03	1.9E-01	AI762391.1	EST_HUMAN	AUT33118 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6518	19863	33054	1.1	1.9E-01	AW148452.1	EST_HUMAN	w54h02.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2394098 3'
7112	18538	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	x14c08.x1 NCI_CGAP_K08 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03659 ATP
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL, PRECURSOR (HUMAN);
7409	20487	33957	0.92	1.9E-01	U73846.1	NT	y809a12.s1 Scores infant brain T1N1 Homo sapiens cDNA clone IMAGE:31683 3' similar to contains MER13
7638	20707	34186	0.78	1.9E-01	U93888.1	NT	repetitive element;
7661	20728	34204	1.39	1.9E-01	U80922.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7708	20773	34258	2.64	1.9E-01	AF072724.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
8174	21259	34778	1.83	1.9E-01	AL161557.2	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
8895	21964	35500	13.56	1.9E-01	AB033024.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
9146	22225	35768	1.5	1.9E-01	M14598.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9146	22225	35769	1.5	1.9E-01	M14598.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	Marsupial cat beta-globin gene mRNA, partial cds
10447	23482	37090	0.81	1.9E-01	BE830353.1	EST_HUMAN	o86g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537508 3' similar to contains Alu
10474	23482	37091	0.81	1.9E-01	BE830353.1	EST_HUMAN	repetitive element;
10890	23965	37593	1.38	1.9E-01	AL161503.2	NT	RC5-E10082-060700-022-A02 ET0082 Homo sapiens cDNA
10890	23965	37594	1.38	1.9E-01	AL161503.2	NT	RC5-E10082-060700-022-A02 ET0082 Homo sapiens cDNA
10892	24071	37704	2.16	1.9E-01	AF223391.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
12026	25009	38711	2.21	1.9E-01	AJ243213.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
12047	25028	38735	1.48	1.9E-01	U73444.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	26274	1.85	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
270	16009	26519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	26625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13946	26993	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1005	14176	27235	1.8	1.8E-01	AF12212.1	EST_HUMAN	w71102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1317	14473	27540	0.87	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1533	14686	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1533	14686	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15068		1.91	1.8E-01	AF733708.1	EST_HUMAN	qp22d10.x5 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	16873		3.34	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-038-q04 DT0018 Homo sapiens cDNA
2863	16140		2.3	1.8E-01	AF184588.1	NT	Jonopodium acaule LEAFY protein (LEAFY2) gene, partial cds
2868	16144	29163	1.19	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2658756 3'
3194	16368	28375	1.61	1.8E-01	AW985178.1	EST_HUMAN	QV6-BN0041-070300-147-q04 BN0041 Homo sapiens cDNA
3452	16819	28638	0.77	1.8E-01	BF163552.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3712	16873	28877	0.87	1.8E-01	H03369.1	EST_HUMAN	y45a01.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3712	16873	29878	0.87	1.8E-01	H03369.1	EST_HUMAN	y45a01.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4453	17593		0.92	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4678	17813	30801	5.61	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4895	18025	31011	2.68	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5129	18254	31219	0.65	1.8E-01	X79794.1	NT	N. tabacum mRNA pNLA-35
5158	18280	31245	1.78	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-q06 ST0203 Homo sapiens cDNA
5206	18327	31297	2.55	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	AI439981.1	EST_HUMAN	i157404.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5291	18409	31376	1.2	1.8E-01	Y08310.1	NT	M.barkeri mlaC and mlaB genes

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.81	1.8E-01	BE082626.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5929	19115	32428	1.19	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
6047	19230	32554	0.95	1.8E-01	N28628.1	EST_HUMAN	Y338108.11 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:284063.5
6256	19430	32776	0.89	1.8E-01	6078428	NT	Mus musculus Trif receptor-associated factor 8 (Trif8), mRNA
6256	19430	32777	0.89	1.8E-01	6078428	NT	Mus musculus Trif receptor-associated factor 8 (Trif8), mRNA
6641	19800	33189	1.16	1.8E-01	Q9QY14	SWISSPROT	PORKHEAD BOX PROTEIN E3
6888	19846		2.12	1.8E-01	N04653.1	EST_HUMAN	Y62702.11 Soares multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:278163.5
7148	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citrus limatus mRNA for vsus, complete cds
7148	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citrus limatus mRNA for vsus, complete cds
7202	20667	33477	0.87	1.8E-01	BE961353.1	EST_HUMAN	601848361R2 NIH MGC_52 Homo sapiens cDNA clone IMAGE:3932247.3
7604	20874	34148	0.81	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21889	35431	0.98	1.8E-01	AW968118.1	EST_HUMAN	EST378191 IMAGE resequences, MAGI Homo sapiens cDNA
9543	22808	36176	1.58	1.8E-01	M73288.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9574	22716	36284	1.62	1.8E-01	9828232	NT	Bacteriophage Ika, complete genome
9892	22741		0.6	1.8E-01	AA468761.1	EST_HUMAN	nf02a05.a1 NCJ CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	repetitive element1
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	S. commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S. commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9881	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9986	23026	36617	0.71	1.8E-01	U87548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.48	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10785	23818	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
10873	23958	37568	2.02	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10917	24000	37633	5	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), duTPase, hollin and lysin genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citrus limatus mRNA for vsus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citrus limatus mRNA for vsus, complete cds
10975	24054	37688	4.41	1.8E-01	AF019107.1	NT	Dictyostellium discoideum unknown (DG1041) gene, complete cds
11270	24338	37978	2.08	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24606	38284	1.41	1.8E-01	AW27528.1	EST_HUMAN	xp40h10.x1 NCJ CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742883.3

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23936	37563	8.94	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
12061	25042	38761	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
12124	25104	38808	1.77	1.8E-01	AA095094.1	EST_HUMAN	cp2798.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086667	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.28	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q96982	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12942	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	y48h10.r1 Soares placenta NE2HP Homo sapiens cDNA clone IMAGE:133027 5'
12988	25643		4.98	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hck1)
13035	28134	31548	1.7	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcobe), mRNA
591	13782	26801	6.4	1.7E-01	BE385184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
828	14006	27063	3.18	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.79	1.7E-01	P35816	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1083	14249	27306	0.89	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1083	14249	27306	0.89	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1880	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
2038	18179		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	18100	28112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and VRAL VIBCO gene, partial cds
2922	18100	28113	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and VRAL VIBCO gene, partial cds
2993	18169	29188	1.47	1.7E-01	AA336909.1	EST_HUMAN	ES141651 Endometrial tumor Homo sapiens cDNA 5' end
3081	18237	29257	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3081	18237	29258	1.09	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3174	18349	29355	1.65	1.7E-01	AF081614.1	NT	Toxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	18818	28637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	18899	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17205	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4881	17816		2.49	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4884	18014	30998	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4981	18090	31066	1.31	1.7E-01	A1247635.1	EST_HUMAN	qh67609.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR.b1 OFR repetitive element;
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 11b (ae) gene, complete cds
6272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827187 5'
5312	18429	31398	0.91	1.7E-01	D37851.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470688.1	EST_HUMAN	net13a02.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470688.1	EST_HUMAN	net13a02.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18903	32188	0.92	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6459	19826	32988	12.64	1.7E-01	H72118.1	EST_HUMAN	yes2q06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6517	19882	33052	0.72	1.7E-01	A1370978.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6517	19882	33053	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6992	18511	31503	0.75	1.7E-01	BE300288.1	EST_HUMAN	600944037T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7019	20155		1.94	1.7E-01	AF026562.3	NT	Mesorcetus auratus oviductin precursor (OVI) gene, complete cds
7140	20275		0.69	1.7E-01	Z82810.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20525	33998	8.51	1.7E-01	BE734179.1	EST_HUMAN	601566022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL58 (HFLFO PROTEIN)
7686	25950	34208	0.64	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8045	21128	34648	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	AF160659.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadL) gene, complete cds
8472	21553	35083	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73KD subunit (CPSF3), mRNA
8472	21553	35084	7.35	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73KD subunit (CPSF3), mRNA
8895	21974	35511	0.5	1.7E-01	AW082873.1	EST_HUMAN	RC2.BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9045	22124	35666	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9188	22276	35814	0.51	1.7E-01	R77002.1	EST_HUMAN	x16602.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9399	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9399	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22828	36407	9.03	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGe resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGe resequences, MAGO Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22856	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9992	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9992	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36845	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C034
10605	23639	37247	1.56	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10607	23641	37249	1.66	1.7E-01	AA627972.1	EST_HUMAN	rq80607.s1 NCL_CGAP_Ca8 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:U25081 TRANSFORMING PROTEIN RHOC (HUMAN);
10918	24002	37636	9.54	1.7E-01	BE330835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11045	24122	37756	2.12	1.7E-01	AA814617.1	EST_HUMAN	6f43a03.s1 NCL_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
11373	24434	38090	6.81	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Ebt1 (Ebt1), mRNA
11373	24434	38091	6.81	1.7E-01	7108300	NT	Mus musculus adenomatous polyposis coli binding protein Ebt1 (Ebt1), mRNA
11657	24736	38427	1.71	1.7E-01	AA883375.1	EST_HUMAN	a45809.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460287 3'
12011	24906		1.5	1.7E-01	P16272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRL LARGE SUBUNIT P51 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRL LARGE SUBUNIT P51 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12587	25920		1.18	1.7E-01	AI824404.1	EST_HUMAN	b68g05.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12907	26800	31972	7.24	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
697	15985	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	y175112.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1561	14703	27783	4.25	1.6E-01	AF268117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1910	15053		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4
1977	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Craosorea gigas RNA polymerase II largest subunit mRNA, partial cds
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	H sapiens mRNA for novel T-cell activation protein
2562	16687	28813	2.73	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2857	16134	29149	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	29889	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3723	16884	29890	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3872	17031	30030	0.82	1.6E-01	AEO00962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.6E-01	AEO04413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4144	17266	30288	1.21	1.6E-01	AF084456.1	NT	Citridia fasciculata tyrosinase I (bnt) gene, complete cds
4448	17688	30569	10.91	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.6E-01	AW968901.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
4586	17723		4.39	1.6E-01	6753319	NT	EST350577 IMAGE Resequences, MAGJ Homo sapiens cDNA
5060	18188	31162	1.39	1.6E-01	AA088343.1	EST_HUMAN	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5083	18211	31183	1.8	1.6E-01	AJ006356.1	NT	218409.51 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:571361 3' similar to TR:E221955
5083	18211	31184	1.8	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5345	18458		0.93	1.6E-01	AF045293.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.6E-01	L40608.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
5639	18833	31909	2.9	1.6E-01	AW197496.1	EST_HUMAN	Lycopersicon esculentum RsaI fragment 2, satellite region
5639	18833	31910	2.9	1.6E-01	AW197496.1	EST_HUMAN	Lycopersicon esculentum RsaI fragment 2, satellite region
5651	18845	32126	1.89	1.6E-01	AF034716.1	NT	Galus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
6152	19328	32674	0.73	1.6E-01	BE925803.1	EST_HUMAN	Galus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
6558	19720	33093	2.06	1.6E-01	AL161588.2	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
6558	19720	33097	2.06	1.6E-01	AL161588.2	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
6939	20252	33688	0.79	1.6E-01	AB046786.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
6985	20213		0.66	1.6E-01	BF9683630.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
7103	18530	31485	4.15	1.6E-01	AW291215.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
7451	20528	34001	0.71	1.6E-01	Z49692.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
7955	21005	34516	1.63	1.6E-01	AW246369.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
7982	21031	34544	0.84	1.6E-01		EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
7986	21035		1.03	1.6E-01	AU136525.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
8063	21136	34657	1.62	1.6E-01	L49346.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
8215	21297		0.53	1.6E-01	BE244087.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
8310	21392	34916	0.77	1.6E-01	U38243.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21812	35450	1.08	1.0E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2987771 to 3213410
9026	22105	35648	0.77	1.0E-01	R13673.1	EST_HUMAN	yf6r08.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28873 5'
9133	22212		0.74	1.0E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35782	1.85	1.0E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR001w
9311	22387		0.78	1.0E-01	AF111672.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.0E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041198-011-h01 ST0200 Homo sapiens cDNA
9854	22894	36475	1.99	1.0E-01	Z49501.1	NT	S cerevisiae chromosome X reading frame ORF YJR001w
9891	22931		1.16	1.0E-01	BE155664.1	EST_HUMAN	PM2-HT0353-270100-004-111 HT0353 Homo sapiens cDNA
10826	23859	37482	0.5	1.0E-01	11128016	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37809	2.34	1.0E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37961	1.34	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37952	1.34	1.0E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37958	1.62	1.0E-01	BE259849.1	EST_HUMAN	601145783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3181183 5'
11377	24438		3.6	1.0E-01	AF108064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24694	38388	7.53	1.0E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12277	25207	38363	3.89	1.0E-01	AV710586.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12697	25402	32043	2	1.0E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12630	25423		1.38	1.0E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12733	25893		11.64	1.0E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurane synthase, complete cds
12833	25815		2.71	1.0E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13029	25878		5.04	1.0E-01	AF287344.1	NT	Fuchsia hybrid cultivar Clu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25880	31864	1.69	1.0E-01	9506522	NT	Rattus norvegicus chondrolectin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13060	25894		1.4	1.0E-01	BE287894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
13189	25782		1.29	1.0E-01	BF672688.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
258	13477	26508	1.7	1.0E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.0E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
600	15884		2.5	1.0E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.0E-01	AL103284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1116	14281	27337	1.44	1.0E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1121	14288	27341	2.7	1.0E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.0E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.0E-01	AW195516.1	EST_HUMAN	nr398f11.xt NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2666085 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27526	3.22	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1511	14664	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
1857	15100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H-B13-ekb-b-09-0-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738641 3'
2980	16168		0.9	1.5E-01	AW572516.1	EST_HUMAN	w556a02.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831878 3' similar to gb:X55072_mel
3100	16278	28280	0.91	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16284	28308	0.62	1.5E-01	O78887	SWISSPROT	Bos taurus factor V, variant 2 (factor V) mRNA, complete cds
3433	16801	28620	5.78	1.5E-01	AA935049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3454	16821	28641	0.73	1.5E-01	Z23104.1	NT	cc68d05.s1 NCL CGAP_GG4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3454	16821	28642	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
							L. signallis mRNA for G protein-coupled receptor
							L. taghali mRNA for G protein-coupled receptor
3851	17011	30011	2.95	1.5E-01	U09694.1	NT	Mus musculus ICR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3887	17028	30025	0.83	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3881	17040	30037	0.77	1.5E-01	M97892.1	NT	XYN1, Thermoanaerobacterium; xynA; 4182 base-pairs
3970	17128	30131	2.45	1.5E-01	AW665883.1	EST_HUMAN	h10006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
3987	17144	30149	0.68	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3987	17144	30150	0.88	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4161	17312	30308	1.16	1.5E-01	AW368659.1	EST_HUMAN	RC2-HT0149-19T099-012-c09 HT0149 Homo sapiens cDNA
4210	17359	30348	0.87	1.5E-01	Z12828.1	NT	B. napus mitochondrion DNA for ORF158
4299	17442	30428	0.85	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4847	17980	30969	1.54	1.5E-01	BF687685.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4068223 5'
4874	15891	28002	2.33	1.5E-01	BF69381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5114	18242	31207	1.5	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5370	18573	31441	1.91	1.5E-01	P07995	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5399	18601	31571	1.33	1.5E-01	AF256652.1	NT	Caenorhodopus MHC class II beta chain (hclbeta) gene, complete cds
5443	18943		5.95	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5655	18949	32131	4.9	1.5E-01	AW850754.1	EST_HUMAN	IL3-C10219-160200-064-F10 C10219 Homo sapiens cDNA
5697	18991	32182	6.66	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5697	18991	32183	6.66	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6028	19212	32632	0.82	1.5E-01	4508810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32647	1.71	1.9E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6128	19307	32648	1.71	1.9E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6168	19344	32690	2.19	1.9E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32852	3.49	1.9E-01	BE727698.1	EST_HUMAN	60156432F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.98	1.9E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19841	33002	1.74	1.9E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6831	20628	33179	3.68	1.9E-01	AE001036.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6881	19820	33207	4.73	1.9E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
6872	19831	33220	1.51	1.9E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33287	2.35	1.9E-01	Q28492	SWISSPROT	AMELOGENIN
6823	19876	33383	0.86	1.9E-01	AA714780.1	EST_HUMAN	nc30410.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6862	20005	33414	2.24	1.9E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31600	6	1.9E-01	AW070295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
7158	25840		0.8	1.9E-01	AA811545.1	EST_HUMAN	gb73102.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:13370719 3' similar to contains element LTR2 repetitive element
7366	20444		4.73	1.9E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20622	34099	1.63	1.9E-01	A973157.1	EST_HUMAN	w52a08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.9E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.9E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7776	20832	34322	1.68	1.9E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-405-Q-UJ11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7776	20832	34323	1.68	1.9E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-405-Q-UJ11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7819	20970	34477	0.79	1.9E-01	U46660.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of ts1-1 (SOL3) gene, complete cds
8248	21330	34846	0.69	1.9E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21466	35028	1.1	1.9E-01	AA870317.1	EST_HUMAN	cc85g12.s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M28062
8507	21588		1.08	1.9E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8594	21676		14.14	1.9E-01	C16800.1	EST_HUMAN	60151052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.9E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (a6572) Homo sapiens cDNA clone GEN-528H09 5'
8793	21872	35411	2.17	1.9E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
8814	21893		0.78	1.9E-01	P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR
8038	22117	35660	3.12	1.9E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9305	22381	35932	2.56	1.5E-01	N74226.1	EST_HUMAN	z559e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298866 3' similar to
9394	22469	36033	1.34	1.5E-01	BF585465.1	EST_HUMAN	PIRS44443 S44443 RAD23 protein homolog2 - human ;
9401	22475		2.62	1.5E-01	AV754819.1	EST_HUMAN	GV000404 Human Psoriasis Differential Display Homo sapiens cDNA
9605	22660		0.84	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAB12 5'
9652	21095	34609	6.7	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3C00080 5'
10022	23060						Adipenser transmontano vitellogenin mRNA, partial cds
10125	23163	36656	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 6-delta - 4-delta isomerase gene, complete cds
10125	23163	36761	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10125	23163	36762	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.69	1.5E-01	X68552.1	NT	P. leniusculus mRNA for integrin beta subunit
10495	23530		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37161	2.36	1.5E-01	AI814046.1	EST_HUMAN	wk53112.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10516	23551	37162	2.36	1.5E-01	AI814046.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10598	23633	37242	1.22	1.5E-01	U40632.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10761	23784	37413	1.69	1.5E-01	AJ011984.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds.
10761	23784	37414	1.69	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10935	24017	37649	1.87	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10935	24017	37650	1.67	1.5E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11063	24139	37773	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11063	24139	37774	4.46	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11925	24911		1.34	1.5E-01	AI193704.1	EST_HUMAN	qe72401.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
12232	25053		38.98	1.5E-01	BF700582.1	EST_HUMAN	gb:MI17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12626	25422		1.84	1.5E-01	AF030358.2	NT	G02128753F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4285549 5'
12633	25426		1.23	1.5E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12696	25978		6.64	1.5E-01	R83077.1	EST_HUMAN	Mus musculus mRNA for death inducer-obliterat-1 (Dio-1)
12749	25498		1.52	1.5E-01	AP001514.1	NT	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194450 5'
12778	25520	32002	1.41	1.5E-01	9695473	NT	Bacillus halodurans genomic DNA, section 8/14
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	Lymphocystis disease virus 1, complete genome
12932	25896	31857	7.68	1.5E-01	AL139074.2	NT	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
							Campylobacter jejuni NCTC11168 complete genome; segment 1/8

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13183	25769	31932	6.61	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	28138		2.28	1.5E-01	8631284	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13828		1.23	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TORBY856P to TORBY21S2A2 region
933	14108		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1288	14444		2.86	1.4E-01	T81884.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.46	1.4E-01	687860	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1954	15097		1.27	1.4E-01	AW13741.1	EST_HUMAN	U1H-B11-acf-a-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720615.1	EST_HUMAN	nv72407.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2544	16669	28703	1.02	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2853	15957	28077	3.34	1.4E-01	A1633496.1	EST_HUMAN	wm74601.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4289	17434	30421	9.45	1.4E-01	A1698094.1	EST_HUMAN	b66602.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4288	17434	30422	9.45	1.4E-01	A1698094.1	EST_HUMAN	b66602.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4362	17465	30476	4.28	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4631	17669		0.7	1.4E-01	AA776287.1	EST_HUMAN	z150x01.s1 Soares fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb-X01057.mai1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4798	17933	30920	0.79	1.4E-01	5433861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (duraea (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
5322	18436	31406	0.62	1.4E-01	AJ005180.1	NT	Lycopodium obscurum genomic RAPD band 26
5421	18822	31598	5.21	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Sitratogene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18844	31621	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18844	31622	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6427	18595	32861	3.17	1.4E-01	BE326891.1	EST_HUMAN	hr87602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135638 3'
6611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6611	19771	33162	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6701	19889	33249	3.7	1.4E-01	AW082706.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6716	19873		1.61	1.4E-01	BE266536.1	EST_HUMAN	601193623FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19895	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	QV1-JM0036-080300-103-403 UM0036 Homo sapiens cDNA
7276	20359		0.71	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0810.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0810 5'
7645	20617		1.78	1.4E-01	AW016373.1	EST_HUMAN	U1H-B10-aat-c-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20888		0.73	1.4E-01	A1762827.1	EST_HUMAN	wf04112.x1 NCI_CGAP_Q111 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P48662 CASPASE-4 PRECURSOR;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20691	34167	0.63	1.4E-01	T83770.1	EST_HUMAN	ya00f11.2 Stragene placenta (#337225) Homo sapiens cDNA clone IMAGE:88973 6' similar to contains
7799	20856	34345	0.95	1.4E-01	U85945.1	NT	Alu repetitive element
7832	20982	34490	1.02	1.4E-01	A1305192.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8162	21244		0.54	1.4E-01	BF310258.1	EST_HUMAN	cl00b12.x1 Soares_NhMMPu_S1 Homo sapiens cDNA clone IMAGE:1879563 3'
8870	21750		1.32	1.4E-01	AV659047.1	EST_HUMAN	601864760F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
8984	22063		0.6	1.4E-01	A1436093.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
9114	22193	35738	4.94	1.4E-01	AA307073.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
9194	22272	35810	0.76	1.4E-01	AW023838.1	EST_HUMAN	TR:002710 002710 GAG POLYPROTEIN. ;
9322	22398	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	EST178182 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	df58603.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9388	22483	36027	8.52	1.4E-01	BF310959.1	EST_HUMAN	W10R05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9475	22532	36096	1.72	1.4E-01	W93411.1	EST_HUMAN	y10r05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	601835465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9547	22612	36181	0.54	1.4E-01	X73293.1	NT	z89404.r1 Soares_fetal_haart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9558	22623	36194	1.65	1.4E-01	Y10195.1	NT	element KER repetitive element:
9558	22623	36195	1.65	1.4E-01	Y10195.1	NT	M.vannelli genes rpoH, rpoB and rpoA
9649	21092	34007	1.51	1.4E-01	AF121361.1	NT	M.vannelli genes rpoH, rpoB and rpoA
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	Homo sapiens PHEX gene
10192	23229	36821	0.89	1.4E-01	AF023813.1	NT	Homo sapiens PHEX gene
10293	23328	36931	0.81	1.4E-01	AW021908.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la (AL), and
10293	23328	36932	0.81	1.4E-01	AW021908.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10463	23498	37109	0.76	1.4E-01	BF375285.1	EST_HUMAN	C.perfringens ORF for putative membrane transport protein
10463	23498	37110	0.76	1.4E-01	BF375285.1	EST_HUMAN	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10680	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	partial cds
10825	23858	37481	0.7	1.4E-01	Z99117.1	NT	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
11081	24156	37793	2.67	1.4E-01	R53400.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
11282	24348	37885	1.69	1.4E-01	AW104982.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
11354	24416	38071	1.68	1.4E-01	T86102.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
							y47403.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111366 5'
							Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
							oa99a03.s1 NC_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
							y77c05.r1 Soares breast 2NBHBT Homo sapiens cDNA clone IMAGE:154088 5'
							xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							y47g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11354	24418	38072	1.58	1.4E-01	T98102.1	EST_HUMAN	ye47g10.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11358	24418	38075	2.36	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11372	24627	36306	1.85	1.4E-01	X68092.1	NT	C. parvovirus ORF for putative membrane transport protein
11613	20817		1.57	1.4E-01	AW016879.1	EST_HUMAN	U1A-B10-eat-c-09-0-L1.st NC1 CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	M. musculus p18K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H6AR (H6ar) gene, complete cds
12560	25382	32038	4.88	1.4E-01	X74773.1	NT	P. salina plastid gene secY
12574	25390		3.28	1.4E-01	11988117	NT	Rattus norvegicus deamin (Dea), mRNA
12605	25405		1.71	1.4E-01	BE864835.2	EST_HUMAN	801658480R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885671 3'
12627	26175		2.83	1.4E-01	BE513802.1	EST_HUMAN	801315538F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3534329 6'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12742	25483		4.02	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12834	25193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12828	25612		1.45	1.4E-01	X69182.1	NT	V. plantifolia mRNA for methyltransferase
13084	25977		3.35	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25765		1.88	1.4E-01	AW377998.1	EST_HUMAN	MRQ-H10208-221299-204-c08 H10208 Homo sapiens cDNA
332	13546	26576	2.27	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 60 (GPR60) mRNA
332	13546	26577	2.27	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26769	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13839	26866	2.43	1.3E-01	AJ277806.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
653	13839	26867	2.43	1.3E-01	AJ277806.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
867	14043	27108	1.55	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27157	1.28	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1052	14218	27274	2.14	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27482	1.87	1.3E-01	AV1712467.1	EST_HUMAN	AV1712467 DCA Homo sapiens cDNA clone DCAAF05 5'

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14828		0.97	1.3E-01	AF148277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Col1a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Bolivitis chierae strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.09	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum adductin pucB5, pucA6, pucB6, pucA7, pucB8, pucA9 and pucC genes and ORF151
2364	15495		1.38	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191098-032-012 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2853	15776	28889	2.78	1.3E-01	M88918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3440	16608	29626	1.21	1.3E-01	AF195779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3816	16976	29979	0.85	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (117)
3818	16976	29980	0.85	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (117)
3822	16982	29985	1.55	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodiphenylhydrolase 4 [AKR 1C4], exon 2
3905	17064	30063	0.66	1.3E-01	6978840	NT	Rattus norvegicus Fibronectin, gamma polypeptide (F99), mRNA
4098	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	13839	28866	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4162	13839	28867	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV9-DT0018-091299-038-a03 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF028805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	XV2310.X1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL169280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4501	17736	30717	0.61	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4556	17792	30776	2.54	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890083 5'
4748	17883	30869	0.73	1.3E-01	BF679694.1	EST_HUMAN	602154308F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.76	1.3E-01	AF000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 984001-1166000 nt, position (517)
5440	18640	31619	1.01	1.3E-01	AW46688.1	EST_HUMAN	ha07608.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM00693-100400-189-a06 UM00693 Homo sapiens cDNA
5616	18812		0.92	1.3E-01	AF107793.1	NT	Emmericella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5702	18895		0.67	1.3E-01	AF056880.1	NT	Hepatitis C virus 68 CL10 genome polyprotein gene, partial cds
5842	18032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32821	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32822	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6698	18856	33246	2.28	1.3E-01	X88891.1	NT	C jacchus intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782928.1	EST_HUMAN	601468957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
6974	20202	33629	0.7	1.3E-01	BE782928.1	EST_HUMAN	601468957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7195	20289		0.74	1.3E-01	BF528560.1	EST_HUMAN	602044345F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7412	20480		1.97	1.3E-01	H48984.1	EST_HUMAN	y33cd2 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8146	21228		0.79	1.3E-01	BE272839.1	EST_HUMAN	601126066F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960083 5'
8160	21242	34762	1.68	1.3E-01	11423294	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
8192	21274	34767	1.32	1.3E-01	BF680522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8469	21650	35080	0.68	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8580	21651		4.96	1.3E-01	8823919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342	1.26	1.3E-01	BF590522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	y39g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	y39g11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9420	22494	36060	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9420	22494	36061	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9672	22834	36204	4.19	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9973	23012		0.73	1.3E-01	N86348.1	EST_HUMAN	J7937F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
10267	23262		1.07	1.3E-01	8353940	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10335	23370	36980	0.95	1.3E-01	AW851599.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
10603	23964	37244	1.08	1.3E-01	AL163246.2	NT	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10743	23776	37389	0.65	1.3E-01	AU121237.1	EST_HUMAN	Homo sapiens chromosome 21, segment H521C046
10787	23830	37454	0.45	1.3E-01	AW247836.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10866	23963		2.31	1.3E-01	BF330999.1	EST_HUMAN	2820637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'
11455	24515		1.34	1.3E-01	BF092708.1	EST_HUMAN	MR4-BT0358-190700-010-h08 BT0358 Homo sapiens cDNA
							MR4-TN0112-120600-102-e08 TN0112 Homo sapiens cDNA

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11529	24585		3.2	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (G12), mRNA
11616	24667	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087048F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11618	24667	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087048F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.98	1.3E-01	BE279449.1	EST_HUMAN	601158032F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24985		1.41	1.3E-01	AF012838.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619364.1	EST_HUMAN	801473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12599	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368		6.39	1.3E-01	AJ242790.1	NT	Gallus gallus seyc1 gene for lymphocidin, exons 1-3
12664	25627		1.31	1.3E-01	AB026828.1	NT	Ephydrata fluvialis mRNA for sALK-6, complete cds
12995	25647		1.87	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares_Dickgraefe_color_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 KIAA0639 PROTEIN. ;
394	13631	26668	13.87	1.2E-01	A421744.1	EST_HUMAN	tt99002.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mel ANNEXIN V (HUMAN);
437	13237		1.42	1.2E-01	U88912.1	NT	Dictyostellium discoideum ORF DG1018 gene, partial cds
561	13763		3.82	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14562	27636	2.32	1.2E-01	AU149149.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001891 3'
1408	14562	27637	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001891 3'
1414	14568		3.35	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
1419	14572		0.94	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1636	14689		0.94	1.2E-01	AA897474.1	EST_HUMAN	ai48909.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1660	14812	27897	1.1	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1682	14834	27919	2.88	1.2E-01	A1285402.1	EST_HUMAN	q66709.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1860553 3'
1808	14957		25.75	1.2E-01	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1970	15113		1.66	1.2E-01	AW449368.1	EST_HUMAN	U14-B13-ak4-e-10-0-J1 st NCI_CGAP_Sub05 Homo sapiens cDNA clone IMAGE:2734554 3'
2253	15386	28514	1.66	1.2E-01	BF248480.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2450	15578		0.99	1.2E-01	Z21405.1	EST_HUMAN	HSAAABZT TEST1, Human adult T cells tissue Homo sapiens cDNA
2656	15779	28803	1.84	1.2E-01	AW396556.1	EST_HUMAN	QV3-BK0046-220300-129-110 BN0046 Homo sapiens cDNA
2905	16083	29098	1.16	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2967	16143	29162	1.9	1.2E-01	A1720470.1	EST_HUMAN	as80c08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3007	16177	29198	3.44	1.2E-01	M18364.1	NT	Human creatine kinase-B mRNA, complete cds
3088	16244	29285	0.91	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.52	1.2E-01	AW370688.1	EST_HUMAN	QV1-BT0259-281099-021-405 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U57600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	16774	29780	1.12	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16733		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3865	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810786RT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4288	17441	30426	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4431	17571	30552	0.69	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. suaveolens mitochondrial ori
5364	18567	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	hy83c04.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5425	18626	31501	2.5	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares, parathyroid_tumor, NBHPA Homo sapiens cDNA clone IMAGE:321689 5'
5484	18683	31700	1.65	1.2E-01	Z98268.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31885	1.14	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE820945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6428	19596	32862	2.26	1.2E-01	AW845275.1	EST_HUMAN	LO-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6483	19659	33022	1.52	1.2E-01	M26625.1	NT	Mouse galactosyltransferase mRNA, complete cds
6581	19723	33101	0.58	1.2E-01	AA747535.1	EST_HUMAN	nx85601.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6785	19940	33338	1.18	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCJ_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158386 5'
7154	20288	33731	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80704.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7154	20288	33732	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80704.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for Interleukin enhancer binding factor 3 (alternative transcripts dbp76, dbp76 gamma, dbp76 alpha and ILF3)
8076	21158		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-009 BN0137 Homo sapiens cDNA
8149	21231	34751	2.45	1.2E-01	AI913753.1	EST_HUMAN	wc88g03.x1 NCJ_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8197	21276	34801	0.64	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
8504	21565	35119	0.68	1.2E-01	AI832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
							at71b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'

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8590	21671		10.78	1.2E-01	AW083852.1	EST_HUMAN	xc49d07.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:MT3452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	35266	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35267	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
8887	21888		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 183 of the complete genome
8920	21899		0.77	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9771	22707	36338	1.3	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
10209	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CHAARE08 5'
11125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11633	24383		3.03	1.2E-01	BE962324.2	EST_HUMAN	60165576R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11593	24646	38284	2.78	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAIL (DNAIL) gene, exon 17
11798	24788	38329	1.72	1.2E-01	R40249.1	EST_HUMAN	Yf80c02.s1 Soares Infant brain (NIB) Homo sapiens cDNA clone IMAGE:28880 3'
12161	25128		2.47	1.2E-01	M65109.1	NT	Rabbit glyoxen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12522	25355		2.09	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12614	26126	31544	4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12732	25486		2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12734	13753		1.65	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12863	25574		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12968	25629	31981	1.4	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12992	25944		4.86	1.2E-01	A1299003.1	EST_HUMAN	gn20g05.x1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1898840 3'
12997	26050		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
13031	25579	31960	6.44	1.2E-01	O96433	SWISSPROT	CYCLIN T
13221	25795		1.47	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
578	13770	26792	1.23	1.2E-01	AF090141.1	NT	Chryseobacterium meningosepticum G0B-1 carboxypeptidase gene, complete cds
630	13915	26838	1.56	1.1E-01	A1561003.1	EST_HUMAN	ht18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
			1.33	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06988_mn1 HEME OXYGENASE 1 (HUMAN);

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1079	14245	27302	1.61	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.65	1.1E-01	AL161660.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1185	18031	27405	3.67	1.1E-01	AW972158.1	EST_HUMAN	EST384142 IMAGE ressequences, MAGL Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D64004.1	NT	Synechococcus sp. PCC6803 complete genome, 23127, 2868787-3002985
1549	14701	27760	2.75	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone IMAGE:2000403 5'
2255	15388		1.73	1.1E-01	AJ006701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2388	15519		2.02	1.1E-01	8755215	NT	Mus musculus pro T-cell antigen receptor alpha (P.tare), mRNA
2803	18959		1.08	1.1E-01	8978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2833	18768		1.27	1.1E-01	AW821809.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2917	18095	29107	0.89	1.1E-01	S62418.1	NT	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
3098	18274	29288	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02.3'
3422	18591		1.55	1.1E-01	8753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenat1g), mRNA
3508	18875	29685	2.09	1.1E-01	BE333188.1	EST_HUMAN	60130876F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	18705	29716	1.47	1.1E-01	X82135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3580	18746	29763	0.71	1.1E-01	R68948.1	EST_HUMAN	y623g08.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element
3673	18838	29846	0.7	1.1E-01	Y07698.1	NT	A.immersus gene for transposase
3791	18852		0.96	1.1E-01	P87384	SWISSPROT	ANNEXIN XI (CALYCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	19981	29965	1.28	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30358	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
4233	17380		0.83	1.1E-01	AF030001.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4367	17510		11.45	1.1E-01	AF157066.1	NT	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4401	17544	30528	0.76	1.1E-01	AW802056.1	EST_HUMAN	Tape-1 integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4762	17897	30877	0.82	1.1E-01	S44957.1	NT	A.immersus gene for transposase
4853	18083	31059	1.23	1.1E-01	Y07699.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5134	17380		0.75	1.1E-01	AF030001.1	NT	mx76a03.a1 NCI_CGAP_Ewt Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5787	18979		2.59	1.1E-01	AA747216.1	EST_HUMAN	

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	19047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32393	0.87	1.1E-01	AL110985.1	NT	Bovine strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32425	0.96	1.1E-01	BF339519.1	EST_HUMAN	602039776F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4166818 5'
5927	19113	32426	0.98	1.1E-01	BF339519.1	EST_HUMAN	602039776F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4166818 5'
5958	19144	32459	1.79	1.1E-01	X88851.1	NT	S. pombe sie8 gene encoding protein kinase
5992	19177	32498	5.15	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6150	19326	32671	1.66	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32693	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-F12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW853698.1	EST_HUMAN	RC3-CT0254-280909-011-a01 CT0254 Homo sapiens cDNA
6554	19716	33092	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6562	19724	33102	1.62	1.1E-01	AF035746.1	EST_HUMAN	AF035749 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg/76008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841089 3'
6742	19898	33289	3.68	1.1E-01	O69335	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19996		2.73	1.1E-01	AF032922.1	NT	Homo sapiens synlaxn 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6934	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7163	20058	33468	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33469	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	28217		1.01	1.1E-01	BF382768.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050863 5'
7466	25845	34007	0.98	1.1E-01	AF000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt, position (6/7)
7706	20771	34255	7.51	1.1E-01	BF694628.1	EST_HUMAN	602140876F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7708	20771	34256	7.51	1.1E-01	BF694628.1	EST_HUMAN	602140876F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20888	34391	2.16	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7872	20926		0.64	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433					afx1b06.s1 Soares_parathyroid_tumor_NGHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
8155	21237	34758	3.06	1.1E-01	AA788784.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.55	1.1E-01	U87492.1	NT	Methanococcus jannaschii section 34 of 180 of the complete genome
8403	21484	35013	1.55	1.1E-01	AA463574.1	EST_HUMAN	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8449	21530	35059	1.26	1.1E-01	X91233.1	NT	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8489	21570		0.94	1.1E-01	AW817918.1	EST_HUMAN	H. sapiens IL15 gene
8546	21627	35185	2.31	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-090200-001-406 ST0270 Homo sapiens cDNA
							DKFZ4547P194.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZ4547P194 5'
							Pedococcus acidilactici H plasmid pSMB74 pediocin Acl production (pap) gene cluster papA, papB, papC
9018	22097	35637	5.67	1.1E-01	U02482.1	NT	and papD genes, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22182	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element.
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.11 Stragena muscle 937209 Homo sapiens cDNA clone IMAGE:927743 5'
9243	22320	35864	2.25	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.11 Stragena muscle 937209 Homo sapiens cDNA clone IMAGE:927743 5'
9335	22411	35964	0.71	1.1E-01	Y12727.1	NT	P. furiosus partial dph5 gene and arg1 gene
9366	22441	36001	2.76	1.1E-01	T72675.1	EST_HUMAN	yd18h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gpM81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.63	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.69	1.1E-01	BE142305.1	EST_HUMAN	CM3-HT0142-271089-026-g11 HT0142 Homo sapiens cDNA
9666	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23162		0.77	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10470	23445		1.23	1.1E-01	R80590.1	EST_HUMAN	YJ6609.e1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147084 3'
10544	23578	37188	1.29	1.1E-01	U60529.1	NT	Ceratitis capitata vovo reobranapocun gag-like, pd-like and env-like genes, complete cds
10914	23697	37631	1.38	1.1E-01	AF245277.1	NT	Dictyostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
11182	24253		2.47	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
11300	24366	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	YJ3611.2.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element.
11483	24542	38212	2.6	1.1E-01	Z11910.1	NT	Z. mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z. mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE602974.1	EST_HUMAN	601876924F1 NIH_MGC 27 Homo sapiens cDNA clone IMAGE:3959608 5'
11586	24639	38319	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24956		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12376	25269		3.78	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12649	25910		3.18	1.1E-01	BE974556.1	EST_HUMAN	601680561R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25758	31947	1.98	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.51	1.0E-01	OB2855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1301	14457	27523	2.18	1.0E-01	AI984499.1	EST_HUMAN	we08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2486577 3' similar to contains MER7.03 MER7 repetitive element.
1423	14577	27650	2.3	1.0E-01	AL151504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2558	15683	28808	1.01	1.0E-01	AW451385.1	EST_HUMAN	UH-B13-alc-d-07-d-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3813	16973	29978	1.11	1.0E-01	BF239818.1	EST_HUMAN	601906489F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134071 5'
4064	17220	30228	2.6	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	17865	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.76	1.0E-01	A1792349.1	EST_HUMAN	ar32d04.y5 Gasler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST304414 MAGE cDNAs, MAGE Homo sapiens cDNA
5261	18380	31346	0.61	1.0E-01	BE389100.1	EST_HUMAN	60128669F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3673552 5'
5436	18636		9.49	1.0E-01	W86490.1	EST_HUMAN	2H62H04.s1 Soares fetal_liver_spleen_infls_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5534	18731		0.87	1.0E-01	X54015.1	NT	X campestris genes for sensor and regulator protein
6001	19186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32893	0.9	1.0E-01	AA481878.1	EST_HUMAN	z441g10.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1 L3 L1 repetitive element
6479	19646	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	z467c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	yH34H06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element
7914	20685		2.39	1.0E-01	Y12488.1	NT	M.musculus wnt gene
8118	21200	34721	0.89	1.0E-01	AA861091.1	EST_HUMAN	ek32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.86	1.0E-01	AW189797.1	EST_HUMAN	x09b01.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S
9387	22462	36026	1.12	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element
9695	22744	36314	0.87	1.0E-01	R44983.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapton mRNA, complete cds
9707	22756		1.9	1.0E-01	M76728.1	NT	y933h04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9790	22888		3.15	1.0E-01	AE001501.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9794	22761	36331	0.55	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J98 section 62 of 132 of the complete genome
10028	23064	36661	1.88	1.0E-01	BF240164.1	EST_HUMAN	z666c10.s1 Soares fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:327282 3'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10351	23386	36995	0.62	1.0E-01	T51952.1	EST_HUMAN	EST369615 MAGE cDNAs, MAGE Homo sapiens cDNA
10537	23572	37179	1.27	1.0E-01	BE792750.1	EST_HUMAN	y628a06.s1 Stragene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3639086 5'
							AU159127 THYROT1 Homo sapiens cDNA clone THYRO1000895 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37991	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4106089 5'
11286	24352	37992	2.17	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4106089 5'
11685	24684	38374	3.64	1.0E-01	BE700543.1	EST_HUMAN	601662558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509952
12364	25633		1.73	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12809	28408		1.73	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12939	25119		3.11	1.0E-01	U52691.1	NT	Gonyalax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12973	25633		1.8	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	28085		25.82	1.0E-01	U68934.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25729		6.58	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13218	28106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2839	15933	28060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster CAMP-dependent protein kinase type II regulatory subunit (pke-Ril) mRNA, complete cds
2847	15981	28070	0.94	9.9E-02	BE545564.1	EST_HUMAN	601070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15961	28071	0.94	9.9E-02	BE545564.1	EST_HUMAN	601070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16513	29528	1.31	9.9E-02	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
7110	18536	31492	8.06	9.9E-02	D83770.1	NT	Aspergillus terreus BSD mRNA for blebistatin S deaminase, complete cds
8098	21181	34699	0.69	9.9E-02	AW103088.1	EST_HUMAN	x443c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
8099	21181	34700	0.69	9.9E-02	AW103088.1	EST_HUMAN	x443c09.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element
9457	22573	36139	1.35	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
12132	25112	38816	3.67	9.9E-02	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
577	13769		2.18	9.8E-02	X56338.1	NT	O. salivaria RAMy3C gene for alpha-amylase
3214	16388	29398	3.66	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7661	20719		0.98	9.8E-02	X54193.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22670		1.16	9.8E-02	M61043.1	NT	Human laminin B1 chain gene, exon 26
11747	23933	37599	1.73	9.8E-02	BF037421.1	EST_HUMAN	601480793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12332	26240		1.29	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14538	27811	1.92	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15466	28601	2.58	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4091	17248		4.05	9.7E-02	Q99796	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18661	31639	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661	31640	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6138	19316	32657	1.39	9.7E-02	AW054476.1	EST_HUMAN	EST366546 MAGE resequencing, MAGE Homo sapiens cDNA
7450	20327	34000	3.05	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	AI953984.1	EST_HUMAN	wk78b06.s1 NCL CGAP_Ox48 Homo sapiens cDNA clone IMAGE:2648747 3' similar to gb:U62851_ma1
11472	24531		1.72	9.7E-02	U55337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2073	15213	28330	1.33	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
2073	15213	28331	1.33	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4464	17604	30582	6.67	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5117	18244	31209	0.95	9.6E-02	AW066230.1	EST_HUMAN	Proteus mirabilis fibrinolytic operon, strain HI4320
6231	19406		2.75	9.6E-02	BE910039.1	EST_HUMAN	EST373303 MAGE resequencing, MAGE Homo sapiens cDNA
8017	21068		0.79	9.6E-02	6678753	NT	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8571	21652		0.65	9.6E-02	AU137084.1	EST_HUMAN	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
9744	22808	36386	1.49	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1006740 5'
10076	23114		1.34	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GK6 Homo sapiens cDNA clone GKCAAH02 5'
10245	23280	36876	1.04	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10245	23280	36877	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.82	9.6E-02	BF07270.1	EST_HUMAN	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10354	23389	36998	1.56	9.6E-02	AB013995.1	NT	602066769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250869 5'
10364	23389	36999	1.56	9.6E-02	AB013995.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10485	23500	37113	3.43	9.6E-02	P08174	SWISSPROT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10961	24060	37694	5.27	9.6E-02	Z76702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD56)
12019	25003	38704	2.8	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
13015	25668		1.7	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
							ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	1.41	9.6E-02	AJ285924.1	NT	Gallus gallus ALPHA 10 nAChR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-F12 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
7455	20532	34006	4.64	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34262	7.77	9.5E-02	AL161638.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7875	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
8064	21146	34666	2.85	9.6E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34667	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	25094		1.82	9.5E-02	7657416	NT	Mus musculus odd Ozien-m homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF212732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
3885	17142	30147	4.64	9.4E-02	Z33059.1	NT	M. capitulum DNA for CONTIG MC073
6447	19614	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7789	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p35 gene, partial cds
8789	21878		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. oyeD, cobQ, sodM, lyeS, rubA, rubB, estB, oxyR, plk, mlgA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p35 gene, partial cds
12214	28011		7.72	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13188	25780	31936	4.84	9.4E-02	U27699.1	NT	Human pepBG1-1 betaine-GABA transporter mRNA, complete cds
3054	16230		2.37	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912526	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESP1), mRNA
3329	18502	29521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289269 5'
4268	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4288	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4857	17990		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAU08 5'
5779	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8442	21523	35052	0.56	9.3E-02	AW56007.1	EST_HUMAN	EST69 Human Fetal Brain MAT CHIMAKER cDNA library Homo sapiens cDNA
8924	22400		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8911	22951	36537	2.3	9.3E-02	BE992631.2	EST_HUMAN	601655688F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23429	37035	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23429	37036	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10526	23561		3.96	9.3E-02	AW206117.1	EST_HUMAN	U1H-B11-afx-h-05-Q-U1 st NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723563 3'
12485	25953		2.08	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
12905	25964		22.03	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
							Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
13139	28010		2.87	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26486	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54156.1	EST_HUMAN	y99807.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3247	16421	26437	3.7	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	29564	1.01	9.2E-02	AA534354.1	EST_HUMAN	rtf9e01 st NCL CGAP_Cc3 Homo sapiens cDNA clone IMAGE:926136 3'
3676	16839		1.14	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctera), mRNA
4353	17466		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980176 5'
4760	17855	30876	3.44	9.2E-02	X96402.1	NT	G. gallus Mia-CK gene
8198	21280	34802	1.82	9.2E-02	T49920.1	EST_HUMAN	y99c08.r1 Stralagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X95266.1	NT	H. vulgare xylose isomerase gene
13120	26201		1.2	9.2E-02	T1468872	NT	Podospira anserina mitochondrion, complete genome
436	13236	26237	2.23	9.1E-02	X77665.1	NT	O. cuniculus K12 keratin gene
3760	18921		0.97	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT03.49-167299-001-602 B10349 Homo sapiens cDNA
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
							Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, GSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, TC7, LST-1, LTB, TNF, and LTA genes, complete cds
5848	19038	32345	1.23	9.1E-02	AF129766.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7459	26218		0.61	9.1E-02	AF029308.1	NT	au74a06.yt Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7546	20618	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	Aeropyrum pernix genomic DNA, section 4/7
7852	20927	34411	0.95	9.1E-02	AP000061.1	NT	Mus musculus thymopolein zeta mRNA, complete cds
7887	20939	34445	1.02	9.1E-02	U39073.1	NT	Homo sapiens gamma adducin gene, exon 9
9124	22203	35746	0.98	9.1E-02	Y14379.1	NT	FB19F10 Fetal brain, Stralagene Homo sapiens cDNA clone FB19F10 3'end
10642	23676		1.46	9.1E-02	T02984.1	EST_HUMAN	Tg616=Cyl actin [T]hpneustes gratilla=sea urchins, embryos, Genomic, 9275 nt]
10874	23708	37316	1.02	9.1E-02	S74059.1	NT	

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-6, G14587-8, and PRL1 genes
11441	24502	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	25121		7.04	9.1E-02	9833494	NT	Bacteriophage Mu, complete genome
12383	28124		1.42	9.1E-02	AA176801.1	EST_HUMAN	z38h12.s1 Stragene muscle 937209 Homo sapiens cDNA IMAGE:611783 3' similar to
12473	26326		1.32	9.1E-02	AF052895.1	NT	SW:TR73_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12998	26954		13.49	9.1E-02	AJ291380.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
13230	26799		1.27	9.1E-02	AF226888.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
						NT	Bombyx mori fibrin heavy chain Fib-H (fib-H) gene, complete cds
763	13844	26980	5.89	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1684	14816	27899	7.33	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2454	16682	28710	1.18	9.0E-02	AW801364.1	EST_HUMAN	IL5-JM0097-240300-030-106 UM0097 Homo sapiens cDNA
2864	15978	28088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15978	28089	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3417	16586	29603	1.11	9.0E-02	AF279135.1	NT	Dichysalium discoidum spore coat structural protein SP65 (cotE) gene, complete cds
4414	17655	30542	0.6	9.0E-02	S88757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4780	17626	30913	2.03	9.0E-02	X85740.2	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
6118	19298	32834	7.2	9.0E-02	W58037.1	EST_HUMAN	Plasmodium falciparum P-type ATPase 3 gene
6880	20012		0.93	9.0E-02	BF062851.1	EST_HUMAN	z69a12.r1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:297694 5' similar to
						EST_HUMAN	repetitive element
12819	25540		1.82	9.0E-02	AF02238.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), EscD (escD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1488	14823	27708	1.25	8.9E-02	BF071593.1	EST_HUMAN	802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1488	14823	27707	1.25	8.9E-02	BF071593.1	EST_HUMAN	802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2460	15597	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251196-003-001 HT0339 Homo sapiens cDNA
4316	17459		1.89	8.9E-02	AF286055.1	NT	Atrichum angustatum AtrichF102 protein (AtrichF102) gene, partial cds
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-alo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088284 3'
5972	19158	32475	2.7	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-alo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088284 3'
5987	19172	32494	3.34	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20423	33886	1.6	8.9E-02	P47289	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN (INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20763		1.77	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pa20F8
8240	21322	34839	1.19	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34832	0.76	8.9E-02	BF701666.1	EST_HUMAN	60212911F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8323	21405	34933	0.76	8.9E-02	BF701665.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8787	21876	35415	5.85	8.9E-02	AA30319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9819	22856	36439	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9819	22859	36440	0.84	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9934	22973	38866	0.63	8.9E-02	AA338366.1	EST_HUMAN	EST144454 Fetal brain 1 Homo sapiens cDNA 5' end
12213	25962		1.8	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12386	25262		3.82	8.9E-02	BF93918.1	EST_HUMAN	602129882F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286180 5'
12637	25366		2.78	8.9E-02	U40493.1	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12584	25393		2	8.9E-02	U28895.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
12827	26199		1.16	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
12880	26133		1.54	8.9E-02	AE001514.1	NT	Helicobacter pylori, strain J99 section 75 of 132 of the complete genome
1404	14588	27632	0.96	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
4012	17169	30177	1.07	8.8E-02	AA299128.1	EST_HUMAN	EST11696 Uterus Homo sapiens cDNA 5' end
4145	17287		5.23	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII-130) (TAFII130)
4418	17539		0.76	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (antridia, keratitis) (PAX6), isoform b, mRNA
7716	20780		0.71	8.8E-02	D17520.1	NT	Sheep mRNA for angiogenesis, complete cds
9188	22268	35807	2.07	8.8E-02	AA151872.1	EST_HUMAN	zn88a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11380	24441	38099	2.79	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11380	24441	38100	2.79	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11541	24597	38273	5.25	8.8E-02	AL040126.1	EST_HUMAN	DKFZp434D1313_r1 494 (synonym: htae3) Homo sapiens cDNA clone DKFZp434D1313 5'
12443	25314	32090	1.19	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
3785	16946	29953	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	18948	29954	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17692	30050	1.4	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5429	18629	31605	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_G031 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18629	31606	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_G031 Homo sapiens cDNA clone IMAGE:701438 3'
6884	20212	33842	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnd1 gene for potassium channel protein, exons 10-14
6884	20212	33843	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnd1 gene for potassium channel protein, exons 10-14
7188	20053	33463	0.57	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8046	21129		0.50	8.7E-02	AA284532.1	EST_HUMAN	z20603.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35328	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10851	24033		2.01	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11591	24644	38326	1.48	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-Ile and tRNA-Ala genes
12431	25308		2.2	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12648	25432		2.85	8.7E-02		NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X65292.1	NT	G. gallus mRNA for vigilin
1281	14437	27506	7.73	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2317	15449	28591	2.2	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3257	19431	29448	2.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3734	18895		3.69	8.6E-02	AF153362.1	NT	Dichoselium discoidium adenyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnp) and prion-like protein (Prnd) genes, complete cds
4809	17746	30726	0.66	8.6E-02	U88179.1	NT	Oryctolagus cuniculus galeodin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	A8011163.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
6219	18394	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19570	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19570	33036	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34308	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8115	21197	34716	1.09	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34860	0.56	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.6E-02	U60168.1	NT	Dicystostellum discoideum proteasome subunit C2 homolog PtiC (ptC) gene, complete cds
9638	22877	36568	1.24	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.6E-02	AW662153.1	EST_HUMAN	h20c08.x1 NCL CGAP_OU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10395	23391	37001	1.07	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37892	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527	24583	38259	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.67	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11875	24863	38559	2.29	8.6E-02	AF283680.1	NT	Bacillus stearotherophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.59	8.5E-02	AE000692.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.66	8.5E-02	N76915.1	EST_HUMAN	yw46h08.t1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:245623 5'
5786	18978	32283	0.73	8.5E-02	AA985491.1	EST_HUMAN	cc83507.s1 NCL CGAP_KH6 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5826	19016		1.99	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6135	19314	32653	6.61	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8805	21884	35424	1.98	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36680	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-O10037-200700-014-605 OT0037 Homo sapiens cDNA
10041	23079	36681	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-O10037-200700-014-605 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X76731.1	NT	V. armodyes gene for armodyoxin C
10702	23735	37340	0.82	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12673	25886		2.76	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
13070	25700		2.44	8.5E-02	AA362834.1	EST_HUMAN	EST72798 Ovary II Homo sapiens cDNA 5' end
2732	16070	28961	4.05	8.4E-02	W69330.1	EST_HUMAN	zc44e11.t1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18927	31603	9.84	8.4E-02	BE267163.1	EST_HUMAN	601180438F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6828	19881	33388	1.46	8.4E-02	AK024468.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8218	21300	34821	6.95	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0780-260400-162-05 BT0780 Homo sapiens cDNA
9043	22122	35664	1.15	8.4E-02	AF218890.1	NT	Homo sapiens atractin precursor (ATRIN) gene, exon 2

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	A1735184.1	EST_HUMAN	as88g10.x1 Barestead colon HPLURB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
10831	23665		0.48	8.4E-02	AV730882.1	EST_HUMAN	O88312 GDB-4. ;
12351	26264	32114	1.67	8.4E-02	R78408.1	EST_HUMAN	AV730882 HITF Homo sapiens cDNA clone HTFBMG04 5'
3682	16845	29853	7.77	8.3E-02	P75334	SWISSPROT	Y63H12.J1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3709	16870	29873	0.75	8.3E-02	A1436787.1	EST_HUMAN	HYPOPHYSICAL LIPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29874	0.75	8.3E-02	A1436787.1	EST_HUMAN	ih82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	8.3E-02	M54964.1	NT	ih82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19558	32917	0.74	8.3E-02	A1942338.1	EST_HUMAN	C.hummi A2b region open reading frame, complete cds
6496	19662	33026	2.87	8.3E-02	AF032663.1	EST_HUMAN	wo79f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8169	21251	34771	3.08	8.3E-02	AF195787.1	NT	Homo sapiens protodactherin 43 gene, exon 1
8202	21284		1.06	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8496	21576		1.31	8.3E-02	AA987873.1	EST_HUMAN	cg85g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1, L1 L1
9738	22803	36377	1.09	8.3E-02	AW583503.1	EST_HUMAN	repetitive element ;
9751	22689		2.02	8.3E-02	AL161955.2	NT	cg85f10.s1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1592779 3'
10549	23584		0.72	8.3E-02	AF020409.1	NT	la05f10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
12448	26128		1.81	8.3E-02	BE958458.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1410	14564		9.13	8.2E-02	Y08170.2	NT	Dicotyledon discoidium DcaA (dcaA) mRNA, complete cds
1525	14678	27759	2.03	8.2E-02	AF167077.2	NT	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'
3141	19317		1.97	8.2E-02	AL163206.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
3904	17063		1.35	8.2E-02	AL161498.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
4114	17268	30268	0.99	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30523	6.58	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4399	17542	30524	6.58	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30525	6.58	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5192	18314	31282	3.43	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5450	18650	31628	1.46	8.2E-02	BE897030.1	EST_HUMAN	Mus musculus zinc transporter (ZnT-3) gene, complete cds
7165	20296	33741	3.16	8.2E-02	AF309555.1	NT	601439676F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7910	20662		0.58	8.2E-02	AV743341.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8805	21984		0.69	8.2E-02	U29397.1	NT	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8971	22050	35503	3.24	8.2E-02	AW876126.1	EST_HUMAN	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9789	22839	36416	4.88	8.2E-02	X04197.1	NT	RC2-P.T0004-Q31298-011-d06 PT0004 Homo sapiens cDNA
							Beet necrotic yellow vein virus RNA-2

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9985	23004	36599	2.27	8.2E-02	BE254318.1	EST_HUMAN	601116055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355586 5'
12454	25318	32094	3.93	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12686	25458	32021	1.43	8.2E-02	AW862186.1	EST_HUMAN	QV4-CT0361-021290-040-b01 CT0361 Homo sapiens cDNA
12909	25875		2.58	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6509	19674	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7756	20815		0.99	8.1E-02	AI692881.1	EST_HUMAN	wd8608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:23386603 3'
8635	21616	35151	0.56	8.1E-02	11428874	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8635	21616	35152	0.59	8.1E-02	11428874	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10116	23154		1.83	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
10885	23719		0.7	8.1E-02	AW289778.1	EST_HUMAN	xv45b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10858	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UHH-B18-ako-g-01-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UHH-B18-ako-g-01-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16003	26246	7.61	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGEC Homo sapiens cDNA
959	14132	27191	0.65	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1733	18046	27074	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1733	18046	27975	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1952	15095	28196	4.4	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-508 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2541	15666		3.21	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2881	14280	27336	1.55	8.0E-02	M23449.1	NT	Dicystidium discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2865	16141	29159	1.05	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3919	17078	30075	0.93	8.0E-02	AW968118.1	EST_HUMAN	EST378191 MAGE resequences, MAGEC Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4935	18065		6.87	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5038	18166	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus salmivirus transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, complete cds, and small nuclear RNAs (snRNAs)
6012	19198	32513	3.59	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19186	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8316	21401	34926	2.41	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9589	22044	36213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, Intron 4
9589	22844	36214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, Intron 4
10361	23366		0.49	8.0E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.84	8.0E-02	AF217796.1	NT	Homo sapiens SOG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38611	1.89	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8) mRNA
12486	25337	32061	3.54	8.0E-02	AJ005376.1	NT	Drosophila arena hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	16376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	800943191 F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3043	18219	28240	12.53	7.9E-02	AI582029.1	EST_HUMAN	ar96c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6881044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30111	4.47	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4902	18082		1.16	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
6836	18989		1.14	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
10234	23269	36859	5.6	7.9E-02	AI081844.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Sm14p (SMT4) gene, complete cds
10234	23269	36860	5.6	7.9E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2
13008	25864		1.27	7.9E-02	AI761639.1	EST_HUMAN	CE08611;
1237	14398	27457	1.49	7.8E-02	AI793276.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2
1237	14398	27458	1.49	7.8E-02	AI793276.1	EST_HUMAN	CE08611;
4915	18045	31035	0.6	7.8E-02	BE836331.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5198	17003		2.97	7.8E-02	BE260048.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7223	20087	33504	1.1	7.8E-02	U62696.2	NT	ou63b05.s1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
							repetitive element;
							repetitive element;
							PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
							800943055 F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2959693 5'
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (Xq28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505		1.1	7.8E-02 U82695.2	NT	Homo sapiens zinc finger protein 92 (ZF92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22064	35604	0.93	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22160	35702	0.89	7.8E-02	X76344.1	NT	S. cerevisiae CAT8 gene
9253	22330	35877	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9561	22703	36269	0.9	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.t1 NCLCGAP_P1 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36637	0.55	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3999281 to 4214814
10901	23985	37616	2.19	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12970	25802	31873	1.35	7.8E-02	U72847.1	NT	Homo sapiens enoipalakin (EYPL) gene, exons 15 through 18
1431	16038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16940		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34690	5.38	7.7E-02	AA402849.1	EST_HUMAN	z453d11.1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
10040	23078	36679	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR099C
10336	23371	36881	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCLCGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10336	23371	36982	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCLCGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24331	37972	3.98	7.7E-02	BE14432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3474	16841	29660	3.1	7.6E-02	BE14432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634803 5'
3494	18861	29673	0.98	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3649	18812	29825	0.96	7.6E-02	AJ400877.1	NT	Homo sapiens ASXL3 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6222	18397	32748	0.89	7.6E-02	AI061276.1	EST_HUMAN	an25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1899730 3'
6486	19653	33015	1.14	7.6E-02	BE378328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10101	23139		0.99	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0645-020800-017-d06 HT0545 Homo sapiens cDNA
10557	23592		1.04	7.6E-02	BE969338.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10815	23848	37469	0.97	7.6E-02	X92656.1	NT	L. esculentum mRNA for tissue phosphate translocator

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	0.97	7.9E-02	X92656.1	NT	L. esculentum mRNA for fructose phosphate translocator
11974	24959	38681	1.93	7.9E-02	AW996045.1	EST_HUMAN	QV3-BN0048-160400-161-604 BN0046 Homo sapiens cDNA
807	13987	27038	1.66	7.9E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13987	27040	1.66	7.9E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1071	15114	28214	0.99	7.9E-02	AL163278.2	NT	Homo sapiens chromosome 21, segment HS21C078
4830	17768	30748	0.74	7.9E-02	AB015961.1	NT	Homo sapiens IL-19 gene for interleukin-18, intron 1 and exon 2
5074	18159	32477	1.45	7.9E-02	AB048714.1	EST_HUMAN	wq24409.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.9E-02	AB64987.1	EST_HUMAN	w152602.x1 NCI_CGAP_Bm28 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN)
8705	21788	35318	1.36	7.9E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10238	23273		0.49	7.9E-02	BF221730.1	EST_HUMAN	7c61cd5.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element MER27 repetitive element ;
10711	23744	37350	0.73	7.9E-02	BF206808.1	EST_HUMAN	801870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10816	23849	37471	0.82	7.9E-02	X79460.1	NT	C.fimi DSM 20113 16S rDNA
490	13684	28718	1.41	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80507, complete genome
2848	15771		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3583	16846	28854	1.21	7.4E-02	AB078865.1	EST_HUMAN	wf43h01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4926	17859	30946	1.10	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4914	18044	31034	2.65	7.4E-02		NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5056	18184	31159	4.42	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchlp), mRNA
6824	19784		1.69	7.4E-02	R17477.1	EST_HUMAN	y914g06.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
6717	19875	33266	0.66	7.4E-02	AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7636	20705	34184	0.84	7.4E-02	AA605132.1	EST_HUMAN	nc71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8085	21167	34683	1.11	7.4E-02	BE880112.1	EST_HUMAN	801493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8809	21779	38312	1.28	7.4E-02	U56089.1	NT	Human periodic tyrophen protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9367	22442	36002	1.08	7.4E-02	AW629605.1	EST_HUMAN	h187d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9367	22442	36003	1.08	7.4E-02	AW629605.1	EST_HUMAN	h187d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9639	21082	34593	0.58	7.4E-02	AB72839.1	EST_HUMAN	w674d02.x1 Scores_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9639	21082	34594	0.58	7.4E-02	AB72839.1	EST_HUMAN	w674d02.x1 Scores_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10019	23057	36653	1	7.4E-02	U62283.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10146	23184	36780	0.49	7.4E-02	BF512878.1	EST_HUMAN	UIH-BW1-amg-g-06-0-J1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069898 3'
11266	24335	37975	1.46	7.4E-02	AA059107.1	EST_HUMAN	z64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
11914	24901	38604	1.42	7.4E-02	AI125083.1	EST_HUMAN	ao11d07.s1 Barstead aorta HPLR63 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86492
12409	26288		1.22	7.4E-02	11626893	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12692	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12870	25580	31995	2.81	7.4E-02	BF030899.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12882	25585	31968	1.44	7.4E-02	AJ23459.2	NT	601453819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3887738 5'
481	13676	26708	1.15	7.3E-02	BE964981.2	EST_HUMAN	Aspergillus nidulans prmJ, prmX, prmA genes
481	13676	26709	1.15	7.3E-02	BE964981.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
702	13885	26917	2.85	7.3E-02	AE001786.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1510	16040	27748	3.26	7.3E-02	AW900281.1	EST_HUMAN	Thermoboga maritima section 101 of 136 of the complete genome
1893	16050		15.79	7.3E-02	AL163302.2	EST_HUMAN	CMQ-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
5112	18240		1.02	7.3E-02	U12283.1	NT	Homo sapiens chromosome 21 segment HS21C102
6682	19744	33126	1.46	7.3E-02	AA779977.1	EST_HUMAN	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7981	21030		0.58	7.3E-02	BF316067.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8361	21442		1.36	7.3E-02	7682107	NT	PROLINE-RICH PROTEIN MP-3
8596	21677	36214	0.5	7.3E-02	Y10887.2	NT	601696047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
9411	22485		1.17	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	Mus musculus cdk5 gene, exon 1, partial
122	13352	26382	0.6	7.2E-02	AE000882.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
122	13352	26383	0.6	7.2E-02	AE000882.1	NT	z24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
1505	14658	27739	2.6	7.2E-02	AL163301.2	NT	gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1505	14658	27740	2.6	7.2E-02	AL163301.2	NT	Melhanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
2614	15738		3.34	7.2E-02	U14794.1	NT	Melhanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
						NT	Homo sapiens chromosome 21 segment HS21C101
						NT	Homo sapiens chromosome 21 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
						NT	Human Immunodeficiency Virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
						EST_HUMAN	UIH-BW0-aj1-a-05-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4465	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18604	31576	2.73	7.2E-02	U67931.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.78	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217598.1	EST_HUMAN	601863905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7318	20400	33663	1.32	7.2E-02	BF216086.1	EST_HUMAN	601863568F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7335	20416	33878	0.7	7.2E-02	AF221128.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	5934897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21463	34987	0.6	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9284	22341		0.57	7.2E-02	V17211.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9881	23000	36596	4.88	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23156	38754	0.96	7.2E-02	BF126399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	h24f11.1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q8Z340 Q8Z340 A TYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10395	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	aa62c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23595	37201	2.15	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10692	23725	37331	5.57	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		3.47	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451550 5'
10837	23870	37492	0.55	7.2E-02	AA706897.1	EST_HUMAN	228105.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451841 3'
11153	24224	37853	4.14	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12318	26230	32104	2.12	7.2E-02	AA773698.1	EST_HUMAN	af81a04.1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	26253		3.63	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12411	26280		2.05	7.2E-02	AA504465.1	EST_HUMAN	nc05h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
12474	26327		4.23	7.2E-02	U62928.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12488	26537		7.37	7.2E-02	AW900962.1	EST_HUMAN	CMA-NN1009-200300-110-c11 NN1009 Homo sapiens cDNA
13048	25687		1.63	7.2E-02	AA401779.1	EST_HUMAN	z57c12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1953	15098	28197	2.05	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene, partial cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2366	15497	28623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082981 5'
8091	21173	34687	1.03	7.1E-02	AI125284.1	EST_HUMAN	q82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738922 3'
10866	23898	37521	0.53	7.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12153	25150		6.48	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3091234 5'
541	13734	26758	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1529	14862		1.28	7.0E-02	X96877.1	NT	MLartella Mibut-1 gene
1601	14950	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	z66f04.s1 Stratiagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3095	16271	29286	2.02	7.0E-02	AA138152.1	EST_HUMAN	UI-H-BIT-acy-c-07-Q-U1.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30167	0.66	7.0E-02	AA815438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 50S
4155	17307	30301	1.19	7.0E-02	BE070284.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4258	17403		1.14	7.0E-02	AW792962.1	EST_HUMAN	CMO-JM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4330	17473	30458	1.19	7.0E-02	AF077821.1	NT	Caris familiaris inducible nitric oxide synthase mRNA, complete cds
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
5493	18982		0.92	7.0E-02	Y08143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7560	20832	34107	0.9	7.0E-02	AV889285.1	EST_HUMAN	AV889285 GK Homo sapiens cDNA clone GKCCAE08 5'
7782	20838	34331	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial aczonin, XL spliced variant (acz gene)
9299	22375	35926	1.24	7.0E-02	9828113	NT	African swine fever virus, complete genome
9797	22837	36415	1.31	7.0E-02	K02801.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
10159	23195	36791	0.88	7.0E-02	U27266.1	NT	Human myosin binding protein H (MYBP-H) gene, complete cds
11654	24733	38424	2.6	7.0E-02	AA724295.1	EST_HUMAN	ah98a05.s1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
13022	25673	31958	1.2	7.0E-02	11421638	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
527	13720	26744	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
527	13720	26745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1364	14518		1.58	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3893	17052	30062	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5302	18419	31389	4.11	6.9E-02	Z76163.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7
7769	20849		0.87	6.9E-02	AF164967.1	NT	M.hydrophilis 115 kDa protein (p115) gene, complete cds
8242	21324		1.14	6.9E-02	U12022.1	NT	Canine distemper virus strain A7517, complete genome
8750	21829	35368	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							601340651F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9320	22396	35949	0.67	6.9E-02	U22967.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38082	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38083	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25251		10.94	6.9E-02	X74315.1	NT	X laevis XFD2 mRNA for fork head protein
12824	25357		1.56	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFc HOMOLOG
12770	25513		3.37	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15075	28178	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1956	15099	28199	3.85	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4575	17810		0.64	6.8E-02	BE141076.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
6758	19914		0.65	6.8E-02	P20792	SWISSPROT	MRO-HT0069-071069-001-c05 HT0069 Homo sapiens cDNA
7040	20093		0.99	6.8E-02	BE061850.1	EST_HUMAN	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7432	20509	33981	8.22	6.8E-02	AL163288.2	NT	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
7881	20915	34420	0.8	6.8E-02	U16856.1	NT	Homo sapiens chromosome 21 segment HS21C068
8483	21564	35098	6.03	6.8E-02	AJ248287.1	NT	Dicostellium discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
12141	28165	35100	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
12276	25206		1.47	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
12906	25589		1.64	6.8E-02	AA758014.1	EST_HUMAN	FB448 Fetal brain, Striatum Homo sapiens cDNA clone FB448 3' end similar to LINE-1
12972	25632		1.34	6.8E-02	AW975839.1	EST_HUMAN	ah67805.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
13203	26091	31660	2.3	6.8E-02	9910585	NT	EST387948 IMAGE resequences, MAGN Homo sapiens cDNA
13588	14711	28186	2.71	6.7E-02	AF155306.1	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1942	15085	28186	2.17	6.7E-02	AJ20285.1	EST_HUMAN	Rattus norvegicus Growth factor independent-1 (GFI1), mRNA
3811	16871	29973	4.48	6.7E-02	P17278	SWISSPROT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
4065	17221	30229	0.74	6.7E-02	U63783.1	NT	ig/9604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
4065	17221	30230	0.74	6.7E-02	U63783.1	NT	HOMEBOX PROTEIN HOX-D4 (HOXA)
7969	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	Cyprinus carpio Rap1b mRNA, complete cds
8034	21117	34635	0.74	6.7E-02	X62695.1	NT	cyprinus carpio Rap1b mRNA, complete cds
							zid2g11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341252 3' similar to contains
							Alu repetitive element; contains element L1 repetitive element;
							H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34636	0.74	6.7E-02	X62695.1	NT	H sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35250	0.73	6.7E-02	AW082688.1	EST_HUMAN	xb81c11.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
8800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B1-1-acr-g-01-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
8900	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B1-1-acr-g-01-Q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1378	14534	27608	0.98	6.6E-02	A1735509.1	EST_HUMAN	at12a09.x1 Bartshead acra HPLR68 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW/LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
2252	15385	28513	3.73	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3552	18717	29731	12.38	6.6E-02	R64306.1	EST_HUMAN	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3667	18732	29748	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3667	18732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	AF260225.1	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5093	18221	31191	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31192	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5130	18255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33254	3.92	6.6E-02	X06411.1	NT	P.vulgaris mRNA for chalcone synthase
6749	19905	33298	0.82	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUEN
6749	19905	33299	0.82	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUEN
6837	19905	33298	0.88	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUEN
6837	19905	33299	0.88	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUEN
8133	21215	34736	1.51	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8669	21749	35287	0.77	6.6E-02	AF009055.1	NT	Dicystotium discoideum dar1 (dar) gene, complete cds
8979	22058		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23194	36790	0.94	6.6E-02	A1458752.1	EST_HUMAN	ig97g06.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
10292	23327	36930	1.5	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar23, rrp22 and bam22 genes
10327	23362		0.85	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.49	6.6E-02	BF694559.1	EST_HUMAN	602080608P2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
11205	24274	37911	4.95	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-008-at12 SN0064 Homo sapiens cDNA
12761	25505		4.84	6.6E-02	9937091	NT	Mus musculus DIPB gene (Dipb), mRNA
13124	25733		1.26	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
695	13785	28805	1.57	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7706088	NT	Homo sapiens E2F-like protein (LOC51270). mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14922	28016	2.04	6.5E-02	AE000784.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5676	18870	32156	2.07	6.5E-02	AA443991.1	EST_HUMAN	zu46h12 s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M25038
6873	19532	33221	0.73	6.5E-02	BF663340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7113	18539	31496	1.02	6.6E-02	U22631.1	NT	602118687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'
10147	23186	36781	0.57	6.5E-02	BE963200.2	EST_HUMAN	Azobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10147	23185	36782	0.57	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3955637 3'
10883	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3955637 3'
10875	23960	37589	4.45	6.5E-02	AA165548.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12163	25129		3.78	6.5E-02	M21469.1	NT	z32g05.a1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12633	25363		3.67	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
589	13780	28789	1.49	6.4E-02	X94548.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
1770	14919	28013	0.99	6.4E-02	AE001777.1	NT	A. canterae precursor of peridinin-chlorophyll-protein (PCP) gene
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
							Thermoboga maritima section 89 of 136 of the complete genome
							q607601.x1 Soares_testis_NHTT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.63
5566	18763	31803	1.11	6.4E-02	A191956.1	EST_HUMAN	LTR8 repetitive element
6239	18413	32761	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6239	18413	32762	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6532	19696	33069	1.23	6.4E-02	A1672696.1	EST_HUMAN	we73g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:39550503 3'
5531	21812		2.47	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 8a (zeta) (Cct8a), mRNA
8865	21844	35478	4.17	6.4E-02	AA093305.1	EST_HUMAN	k1419.seq.F Human fetal heart_Lambda ZAP Express Homo sapiens cDNA 5'
9327	22403	35955	0.98	6.4E-02	AF150185.1	EST_HUMAN	AF150185 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9785	22928		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
9918	22956	36545	1.87	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10468	23503	37118	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10468	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24953	38997	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12008	24963	38698	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12479	25331	32056	2.67	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III region Hec701 gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3682	16864		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6264	19438	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.64	6.3E-02	X67869.1	NT	H.sapiens gene encoding La autoantigen
9491	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster DmTina gene, exons 1-3
10218	23254	36843	3.52	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone GKCAHE01 5'
10954	19438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15874	28787	1.04	6.2E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4365	17508	30489	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17840		5.66	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (ROSS-A)) (RO52)
6935	20250	33885	0.78	6.2E-02	D48530.1	NT	Spirulina platensis DNA for acetylase cyclase, complete cds
7805	20851	34354	0.88	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21067		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	26226		0.92	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.s1 Soares_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9881	22730	36300	1.10	6.2E-02	6877898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2) mRNA
11415	24476	38140	1.42	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Melanizium antisoplae mRNA for Chymotrypsin (chyt) gene
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 108 of the complete genome
12817	25415		1.24	6.2E-02	BE763065.1	EST_HUMAN	601583733F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12703	25457	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	737h08.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
266	13485	26516	3.63	6.1E-02	D16471.1	NT	TR-Q8Y4S6 Q8Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1]; Human mRNA, Xq terminal portion
4099	17264		2.85	6.1E-02	U79325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKG1) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8456	21639	35068	3.65	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21940	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
8861	21940	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834604 3'
10967	24048	37681	3.9	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-138-C06 HT0818 Homo sapiens cDNA
12134	25114	38818	1.66	6.1E-02	AB025933.1	NT	Epiplatys burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26093		30.03	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
12836	25957		1.58	6.1E-02	AI886811.1	EST_HUMAN	U5907.X1 NCL_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2292901 3'
12863	25646		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1291	14447	27513	1.58	6.0E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
2740	15857	28669	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380924 IMAGE resequences, MAGJ Homo sapiens cDNA
2832	15846		1.43	6.0E-02	AB031289.1	NT	Mesocricetus auratus mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	Zp78c04.11 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	Zp78c04.11 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:626310 5'
3301	16475	29496	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3301	16475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3725	16896		0.76	6.0E-02	BE964443.2	EST_HUMAN	601658160R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0263-011199-013-004 BT0263 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	AI607537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 repetitive element:
7127	18553	31467	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7127	18553	31468	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7338	20418	33980	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7857	20912	34417	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf68b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754189 3'
8617	21697		0.48	6.0E-02	11466486	NT	Reclinomonas americana mitochondrion, complete genome
9472	22529	36092	1.29	6.0E-02	AI623167.1	EST_HUMAN	Is78a06.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.29	6.0E-02	AI623167.1	EST_HUMAN	Is78a06.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237362 3'
9806	22651	36233	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9806	22651	36234	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA308797.1	EST_HUMAN	EST180854 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 80 kDa-like

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24659		1.42	6.0E-02	AA123386.1	EST_HUMAN	zn87c08.t1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gp.X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12921	25606		5.12	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:Q60298
239	13461	28489	5.86	5.0E-02	AW934719.1	EST_HUMAN	RC1-DT0001-280100-012-e10 DT0001 Homo sapiens cDNA
3048	16224	29246	2.77	5.9E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4804	17997		0.77	5.9E-02	AF168111.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
8817	21896	36435	2	5.9E-02	9055249	NT	Mus musculus irquois related homeobox 5 (Drosophila) (hxs), mRNA
9650	21093		0.97	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
11026	24104		7.39	5.9E-02	BF572539.1	EST_HUMAN	Mus musculus follistatin-like (Fst), mRNA
11835	24824		1.35	5.0E-02	BF572539.1	EST_HUMAN	602076549F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
11850	24839		1.37	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere function
956	14129		6	5.8E-02	D80110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1693	14845	27929	0.97	5.8E-02	Q81768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3753	16914	29917	1.88	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 139 of the complete genome
4474	17614	30593	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4669	17804	30792	4.64	5.8E-02	AI247505.1	EST_HUMAN	q45601.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30783	4.64	5.8E-02	AI247505.1	EST_HUMAN	q45601.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4696	17831		2.1	5.8E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7855	20910	34414	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7855	20910	34415	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8866	21945	35479	0.61	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12365	25261		1.65	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12681	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	nc75et1.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112884 3'
3123	16298	29312	1.14	5.7E-02	AI081844.1	EST_HUMAN	ou63105.s1 NCI_CGAP_BR2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
3139	16316	29328	1.09	5.7E-02	AF119117.1	NT	CE08611 ;
3902	17061	30060	2.3	5.7E-02	AW988791.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
4807	17941		0.95	5.7E-02	M95098.1	NT	EST378865 MAGE resequences, MAGE1 Homo sapiens cDNA
							Bos taurus lysozyme gene (cow 3), complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.87	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20659	34175	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7630	20699	34176	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7710	20775	34280	0.72	5.7E-02	D78003.1	NT	Xeropus laevis mRNA for fourth component of complement, complete cds
7710	20775	34281	0.72	5.7E-02	D78003.1	NT	Xeropus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
10059	23093	36695	0.82	5.7E-02	6881260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11464	24523	38183	3.14	5.7E-02	A1752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
11464	24523	38184	3.14	5.7E-02	A1752885.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
11030	24710		1.66	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
12586	25969		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12769	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12853	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13012	26165		5.21	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	y6cd10.s1 Soares breast 2NBH-Bst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element;
1556	14709	27789	1.1	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
2362	15493		1.95	5.6E-02	BE904308.1	EST_HUMAN	601484578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898610 5'
4763	17898	30878	1.37	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30936	1.31	5.6E-02	AA290599.1	EST_HUMAN	zz45c01.s1 NCL CGAP GC81 Homo sapiens cDNA clone IMAGE:700416 3'
6789	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	x02c10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O64979 O94979 KIAA0905 PROTEIN;
7031	20167	33589	1.02	5.6E-02	AA868182.1	EST_HUMAN	cd47f12.s1 NCL CGAP GC81 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7301	20383	33842	3.3	5.6E-02	BE008001.1	EST_HUMAN	QY0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
8010	21060	34572	1.32	5.6E-02	AI183883.1	EST_HUMAN	q664g11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35623	2.52	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9002	22081	35624	2.52	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10017	23055	36651	1.18	5.6E-02	AA482864.1	EST_HUMAN	n149d07.s1 NCL CGAP_AV1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.1;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11863	24851		2.42	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	15338	28948	7.33	5.5E-02	X67869.1	NT	H.sapiens gene encoding La autoantigen
3286	16460	29481	3.33	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.5E-02	L41551.1	NT	Gallid herpesvirus mRNA fragment
5776	18668	32272	3.49	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18968	32272	4.32	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.5E-02	6735902	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8311	21393	34917	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21393	34918	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9855	22895	36476	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36477	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9951	22990	36583	1.24	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11271	24339	37677	6.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
3084	16260		0.85	5.4E-02	AJ277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3609	18476		8.19	5.4E-02	BE073463.1	EST_HUMAN	RCS-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4020	17177	30186	0.61	5.4E-02	U88806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8316	21398		1.18	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2619730
9271	22347	35897	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37663	1.86	5.4E-02	U20760.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
12463	25980		3.72	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1535	14668	27768	20.57	5.3E-02	T84769.1	EST_HUMAN	yac712.1 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:119851 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2586	15891	28818	3.22	5.3E-02	AJ276403.1	NT	Pseudomonas putida tgsS gene
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29406	4.83	5.3E-02	AJ276403.1	NT	Pseudomonas putida tgsS gene
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31612	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5434	18634	31613	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6228	19403	32753	1.14	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20160	33580	4.02	5.3E-02	9885413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33760	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7617	20560		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mca, mRNA, 4053 nt]
8061	21073	34585	0.68	5.3E-02	SWISSPROT		HYPOTHEITICAL 130.0 KD PROTEIN IN SNF8-SPO11 INTERGENIC REGION
8000	21681		0.68	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cytalan C (cst3) gene, complete cds
8325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-actin DNA
10462	23497		0.61	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurule, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10538	23573	37180	0.79	5.3E-02	X68432.1	NT	B. retro paulci mRNA for transcription factor
13173	25761	31931	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2358	15488		64.04	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	16356	28363	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	29364	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17208	30216	0.8	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Ner-1 mRNA, complete cds
5287	18406	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32645	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.94	5.2E-02	AB030965.1	EST_HUMAN	wj80e04.x1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element
7424	20501	33972	1.23	5.2E-02	P38322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8389	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9931	22871	36560	2.16	5.2E-02	D10927.1	NT	Turp mosaic virus genomic RNA for Capsid protein, complete cds
9931	22971	36561	2.16	5.2E-02	D10927.1	NT	Turp mosaic virus genomic RNA for Capsid protein, complete cds
12725	25483		1.6	5.2E-02	Q03030	SWISSPROT	OXALACETATE DECARBOXYLASE ALPHA CHAIN
2437	15565		0.88	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
6161	18283	31248	0.89	5.1E-02	BE957423.2	EST_HUMAN	60165356R2 NIH_MGC.55 Homo sapiens cDNA clone IMAGE:38838381 3'
5251	18372		0.96	5.1E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
5349	18482		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	18866	33370	0.79	5.1E-02	AF280388.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6997	18518	31508	1.73	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-p08 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21528	35056	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131968.1	NT	Spodoptera littoralis mRNA for 3-dehydroxydysone 3beta-reductase
9086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36646	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37028	1.9	5.1E-02	P40803	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN OEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487		1.81	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
496	13690	26721	2.8	5.0E-02	AF080004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	4) SALIVARY AGGIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEP TIDE P-C]
2879	14182	27244	10.08	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3418	16887		1.36	5.0E-02	7305610	NT	Mus musculus Uro-S1 like kinase 2 (C. elegans) (Ulk2), mRNA
3664	16647		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3775	16936	28942	5.9	5.0E-02	U12769.2	NT	Arthraea pernyi period clock protein homolog mRNA, complete cds
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
8258	19432	32779	0.84	5.0E-02	AF066284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6438	19605		1.28	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7128	18554	31469	0.58	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7913	20984		0.67	5.0E-02	AW062464.1	EST_HUMAN	MRO-CT0084-100899-002-g10 CT0084 Homo sapiens cDNA
10403	23436	37045	1.37	5.0E-02	AF305238.1	NT	Mus musculus Fae-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
10855	23888		0.55	5.0E-02	BF213280.1	EST_HUMAN	601844753F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4070101.5
11782	24772	38469	2.26	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12229	28004		4.7	5.0E-02	Q04047	SWISSPROT	NO-QN-TRANSIENT A PROTEIN
231	13452		11.82	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	26623	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
380	13588	26624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2937	18114	29126	0.71	4.9E-02	U52698.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3360	18532	29646	1.85	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3660	18623		0.85	4.9E-02	AA188940.1	EST_HUMAN	z448a12.s1 Straigene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
3661	18644	28851	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3662	18644	28852	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4664	18063	31069	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCJ CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4664	18063	31070	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCJ CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5498	18685	31702	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5498	18685	31703	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7282	20374	33831	1.79	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8818	21894		1.07	4.9E-02	AE002308.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.9E-02	BE931532.1	EST_HUMAN	MR0-H10408-170800-003-e08 HT0408 Homo sapiens cDNA
8954	22033	35576	0.97	4.9E-02	AL181559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37459	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24686	38376	3.46	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	28624		3.23	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26582	1.16	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26582	2.61	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13696	26726	11.53	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	28610	2.08	4.8E-02	W51983.1	EST_HUMAN	z448b02.s1 Soares senescent_fibroblasts_NH9SF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb-M30598 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3280	16454	28478	1.78	4.8E-02	X17144.1	NT	Tetrahymena trostrata histone H3l1 and histone H4l1 intergenic DNA
4793	17928		1.08	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle myosin receptor
5237	18359	31328	0.98	4.8E-02	U91814.1	NT	Streptococcus constellatus D-alanine-D-alanine ligase gene, partial cds
8532	21414	34940	1.41	4.8E-02	AW388497.1	EST_HUMAN	MR2-S10128-221099-012-b02 S10128 Homo sapiens cDNA
9329	22405	36957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	36958	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24286	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
11219	24286	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.8E-02		9632893	Streptococcus thermophilus bacteriophage Sfi19, complete genome
6122	18248	31214	0.74	4.7E-02		6981281	Rattus norvegicus Neslin (Nes), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6969	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	y29709.t1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
7025	20161	33581	0.69	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.69	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M82752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8445	21626	35053	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB026978.1	NT	Gallus gallus Wpki-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9936	22875		0.7	4.7E-02	A1873042.1	EST_HUMAN	we9c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11862	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLO Homo sapiens cDNA clone GLOBKD02 3'
281	13499	26531	0.69	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13539	26584	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476		1.49	4.6E-02	A014255.1	EST_HUMAN	am50402.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1390	14644	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA contains element LTR1 repetitive element ;
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTG Homo sapiens cDNA clone HTGBW C01 5'
2859	13499	26531	1.78	4.6E-02	BE153583.1	EST_HUMAN	xn24f03.x1 NCL OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
3073	16249	29270	0.64	4.6E-02	BE153583.1	EST_HUMAN	Q12846 G-RICH SEQUENCE FACTOR-1 ;
3410	16249	29270	0.59	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3985	16249	29270	0.94	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4236	17365		0.82	4.6E-02	AF220365.1	NT	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5852	19042	32348	1.57	4.6E-02	AF075982.1	NT	Mus musculus nuclear RNA helicase II(Gu ddx21) gene, complete cds
6359	19529	32887	3.87	4.6E-02	X61624.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6938	20251	33687	1.41	4.6E-02	A1149574.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
8007	21057	34569	0.83	4.6E-02	6978720	NT	q60b008.x1 Soares_placenta_86c8weeks_2N8HP806W Homo sapiens cDNA clone IMAGE:1719371 3' similar to contains L1 L1 repetitive element ;
8856	21855	35472	3.81	4.6E-02	BE154008.1	EST_HUMAN	Rattus norvegicus Cathespin H (CstH) mRNA
11689	24887	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-050400-009-G12 HT0339 Homo sapiens cDNA
							d127109.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13078	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
460	13653	26983	2.24	4.9E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.6E-02	AF005730.1	NT	Marburg virus strain MS.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1245	14404	27466	1.52	4.6E-02	AF005730.1	NT	Marburg virus strain MS.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1847	14653	28095	4.83	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3817	16977	28981	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6380	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C080
6636	18796	33184	0.84	4.5E-02	AL163280.2	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
7018	20154	33574	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
7018	20154	33576	0.59	4.5E-02	L28487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene; carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
8587	21668	35207	2.24	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAA1-box binding factor HAP3 homolog gene, complete cds
10155	23192	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to similar to neuro-D4 protein
10305	23340	36946	0.47	4.5E-02	X95508.1	NT	A. europaeum mRNA for legumin-like protein
10421	23456	37061	0.79	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12442	28313	32089	2.61	4.5E-02	11418013	NT	Homo sapiens ret finger, protein-like 3 (RFPL3), mRNA
12891	26081	31694	3.79	4.5E-02	AA191097.1	EST_HUMAN	z43f11.1 Stratagene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:632483 5'
227	13449	27273	4.35	4.4E-02	BE972733.1	EST_HUMAN	601562164F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
1050	14216	27273	0.77	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2163	15289	33803	6.82	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2559	15694	28809	1.81	4.4E-02	AW878475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3730	16881	28895	1.68	4.4E-02	AF159160.1	NT	Mycobacterium xenopus seipin/threonine kinase Plk10 (plk10) gene, complete cds
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30866	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7267	20350	33802	0.59	4.4E-02	AF098824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7267	20350	33803	0.59	4.4E-02	AF098824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA736969.1	EST_HUMAN	nt13023.s1 NCL_OGAP_SST1 Homo sapiens cDNA clone IMAGE:1238221 3'
11328	24389	38034	2.64	4.4E-02	AF060698.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24336	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	aa33304.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12158	25126		4.55	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1463 protein, partial cds
12347	26182		1.85	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
802	13962	27034	7.26	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	28871	1.55	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3516	16882	29663	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21G010
3749	16910		1.21	4.3E-02	AF080568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6625	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6626	19785	33173	4.84	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA652266.1	EST_HUMAN	ns89c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886
8711	21791	35327	0.69	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35621	1.32	4.3E-02	X53322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	22080	35622	1.32	4.3E-02	X53322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25281		1.2	4.3E-02	AL138077.2	NT	Campylobacter jejuni NCTC11189 complete genome; segment 4/6
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
889	14085		2.4	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
919	14094	27158	1.51	4.2E-02	AW003845.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q83291 Q83291
1759	14907		1.37	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA; contains L1.13 L1 L1 repetitive element;
1818	14868	28080	0.99	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3754	18915	28918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4885	17998	30982	0.59	4.2E-02	BF342395.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
							602017105F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4152672 5'
5735	18028	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE288285.1	EST_HUMAN	601124566F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2988319 5'
7695	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34267	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9010	22089	39631	3.82	4.2E-02	PO5095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN PROTEIN 1) (TBR-1) (TES-56)

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11295	24381	38002	1.52	4.2E-02	AA978118.1	EST_HUMAN	at33b1.1 s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24640	38320	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11587	24640	38321	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11795	24785	38483	1.52	4.2E-02	AF178458.1	NT	PRRS isolate PRRSV/36 envelope glycoprotein gene, complete cds
12729	26109		6.64	4.2E-02	AI983494.1	EST_HUMAN	w449g10.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
13078	25705		1.17	4.2E-02	D14711.1	NT	Staphylococcus aureus HSP10 and HSP60 genes
523	13716	26743	1.86	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2741	15858	28970	1.06	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533333 5'
4005	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533333 5'
4595	17732		6.4	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-194-f08 NN0012 Homo sapiens cDNA
5229	18351		0.91	4.1E-02	X85880.1	NT	L monocytogenes type 3 partial lap gene (strain 443)
5759	18851	32253	1.06	4.1E-02	BE251694.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5759	18851	32254	1.06	4.1E-02	BE251694.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
7022	20158		0.98	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7882	20747	34228	1.78	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (d beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20892	34502	2.81	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
8402	21483	35011	0.74	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8845	21924	35482	0.79	4.1E-02	P34887	SWISSPROT	MOTIFS 1 (ADAMTS-1) (ADAM-TS1)
8355	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	CUTICLE COLLAGEN 34
13112	26110	31666	9.91	4.1E-02	AJ271909.1	NT	EST 84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3316	16489	28507	3.85	4.0E-02	AB040604.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3900	17059	30058	1.08	4.0E-02	L11910.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
							Human retinoblastoma susceptibility gene exons 1-27, complete cds
5495	18894	31710	5.31	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	19513	32870	0.98	4.0E-02	BF110494.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:075296 075296 R29124_1;
7867	20921	34428	5.99	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7929	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20953	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20953	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7980	21029	34543	0.61	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte topomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9844	22884		0.63	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9869	22909	36495	2.48	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thio: fumarate reductase subunit A
10190	23227		1.08	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Car+ ATPase
12333	25908	31859	16.34	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1144	14309	27366	2.79	3.9E-02	BF516149.1	EST_HUMAN	UHL-BW1-enx-h-08-0-U1st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1375	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2016	15156	28261	3.22	3.9E-02	AJ403386.1	NT	Musculus DNA for desmin-binding fragment DesD7
2769	15884		1.97	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd (SDHC) mRNA
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 S10258 Homo sapiens cDNA
5276	18398	31368	0.9	3.9E-02	8924079	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5279	18398	31367	0.9	3.9E-02	8924079	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5949	19039	32346	1	3.9E-02	BE968841.1	EST_HUMAN	601649674F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
5977	19162	32482	0.85	3.9E-02	BF676203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7203	20068	33478	0.87	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8023	21106	34823	1.44	3.9E-02	BF238613.1	EST_HUMAN	601908948F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8250	21332	34849	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11693	21071	34552	1.56	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	25039		3.54	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12898	25595		2.35	3.9E-02	U60061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV4S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
13036	25979		64.99	3.9E-02	AL049893.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnx2.2borf
5556	18374	31792	0.8	3.9E-02	M11228.1	NT	Human protein C gene, complete cds
6212	18387	32736	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-34 (HOX-2.6)
7471	20548	34018	1.72	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8864	21943		1.51	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10789	23822	37446	0.84	3.8E-02	7662563	NT	Homo sapiens PRO0514 protein (PRO0514), mRNA
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1016	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2310	15442	28577	6.19	3.7E-02	A1894806.1	EST_HUMAN	wf85608.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2845	15768	28893	0.97	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3115	16291	29306	1.13	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3117	16293	29307	4.33	3.7E-02	BF312963.1	EST_HUMAN	601856233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3543	16708		0.91	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcma3), mRNA
7226	28216		0.95	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 517
7868	20923	34430	0.81	3.7E-02	AE003975.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
10218	23255		1.01	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares_parathyroid_tumor_NSHPA Homo sapiens cDNA clone 1360912 3'
12227	25178	38837	7.41	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12681	25945	31764	3.71	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
13089	25699		1.23	3.7E-02	11467432	NT	Odontella aeneasis chloroplast, complete genome
3744	16905	29809	0.82	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3752	16913	29916	0.9	3.6E-02	AL099806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL099810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5543	18740	31759	0.81	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	0.86	3.6E-02	AF181722.1	NT	Homo sapiens RU2AS (RU2) mRNA, complete cds
6846	19989	33408	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6846	19989	33408	4.48	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cys2 precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	nm2005.s1 NCI CGAP GC50 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7811	20866	34360	0.94	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9591	22646	36216	2.16	3.6E-02	U20608.1	NT	MRQ-HT0158-030200-003-508 HT0158 Homo sapiens cDNA
9591	22646	36217	2.16	3.6E-02	U20608.1	NT	Dicystostellum discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.84	3.6E-02	BF347586.1	EST_HUMAN	Dicystostellum discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
11456	24516	38183	1.49	3.6E-02	BF131609.1	EST_HUMAN	602020453F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
11456	24516	38184	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14093	27158	0.99	3.6E-02	U09506.1	NT	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
1033	14202	27280	2.43	3.6E-02	AF253417.1	NT	Drosophila melanogaster figgrin mRNA, complete cds
1595	14748	27831	1.4	3.6E-02	BF678085.1	EST_HUMAN	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1695	14748	27832	1.4	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.6E-02	AE001773.1	NT	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4435	17575	30556	1.11	3.6E-02	P53780	SWISSPROT	Thermotoga maritima section 85 of 136 of the complete genome
6351	19521	32876	1.76	3.6E-02	J01238.1	NT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
8165	21247		0.91	3.6E-02	H29851.1	EST_HUMAN	Maize actin 1 gene (Mact1), complete cds
8824	21903	36443	2.53	3.6E-02	BE969070.1	EST_HUMAN	yp-44a05.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
10224	23260	38848	0.94	3.6E-02	X76842.1	NT	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
10270	23305	36902	0.61	3.6E-02	BE561042.1	EST_HUMAN	L. lactis MG1363 grpE and drak genes
11785	24775	38471	1.79	3.6E-02	AW861641.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775	38472	1.79	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12876	25583		1.31	3.6E-02	AF009883.1	NT	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
12955	25991		2.71	3.6E-02	BE276948.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
592	13783	26802	47.29	3.4E-02	AK024424.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S8P to TCRBV21S2A2 region
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3549883 5'
593	13783	26802	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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593	13783	26803	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1076	14242	27268	2.57	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW: C211_HUMAN P63801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1233	14392		5.43	3.4E-02	11346459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	ye20e06.r1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3517	16883	29694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE639574.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4030	17188	30198	3.72	3.4E-02	AW794952.1	EST_HUMAN	RG6-UM0018-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17895	30838	2.77	3.4E-02	X59799.1	NT	Musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Ceenorhabditis elegans mRNA for DYS-1 protein, partial
6883	18512	31504	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8456	21537		3.15	3.4E-02	AI869629.1	EST_HUMAN	wf86d04.x1 NCI_CGAP_Alvi CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35567	1.18	3.4E-02	AA664886.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_Alvi CGAP_Brm25 MER25 repetitive element ; element contains element MER25 MER25 repetitive element ;
9118	22197		5.28	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.e1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9980	23019		0.86	3.4E-02	AI082719.1	EST_HUMAN	(P)SGKPLPKVTLSDGVPKATMRFNTEITAENL.TINLKESVTADAGRYEITAANSSGTTKAFINIVLDRPG
383	13581		6.8	3.4E-02	AA398735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYGDSQVNYLLKRETSATVWTEVSATVARTMMKVKML ... ;
1183	14355	27413	12.43	3.3E-02	AB038667.1	EST_HUMAN	ca58h08.x1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1668	14821	27904	1.23	3.3E-02	AF110763.1	NT	z75e08.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1778	14927		1.37	3.3E-02	AE000700.1	NT	Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2149	15285		2.02	3.3E-02	R09112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
3445	16613	29631	0.86	3.3E-02	H02389.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
4293	14821	27904	3.74	3.3E-02	AF110763.1	NT	yf28c08.r1 Soares_fetal_liver_spleen_TNFSL Homo sapiens cDNA clone IMAGE:127888 5'
4589	17726	30709	2.24	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
6500	19722	33099	25.73	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
8560	19722	33100	25.73	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7877	20742	34223	0.63	3.3E-02	AF124182.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8523	22588	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana glumabagittalia molycoprotein synthase sulphuryase (crtX5) gene, partial cds
8523	22588	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:3562423 3'
8523	22588	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:3562423 3'

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9824	22879	36248	0.67	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9824	22879	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11393	24444	38104	3.28	3.3E-02	BF691107.1	EST_HUMAN	ad08f09.s1 Soares NBHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
12428	25303		3.1	3.3E-02	T96645.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12557	25379		1.6	3.3E-02	AF289666.1	NT	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:121101 5'
12591	25398		1.85	3.3E-02	M81890.1	NT	ye49f11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
134	13360	26394	1.79	3.2E-02	AJ002005.1	NT	Mus musculus E1F4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
1150	14314	27370	6.32	3.2E-02	AF096275.1	NT	Oryzotagus cuticulus gene encoding ileal sodium-dependent bile acid transporter
1150	14314	27371	6.32	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1812	14961	28054	1.08	3.2E-02	AF128864.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2902	13360	26394	0.87	3.2E-02	AJ002005.1	NT	LARGE TEGUMENT PROTEIN
3204	16378	29389	13.21	3.2E-02	BE887353.1	EST_HUMAN	Oryzotagus cuticulus gene encoding ileal sodium-dependent bile acid transporter
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	801442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
4334	17477		16.42	3.2E-02	X64768.1	NT	Homo sapiens chromosome 21 segment HS21C003
4890	18020	31006	3.85	3.2E-02	AF114182.1	NT	H.sapiens RFP3 gene (XLRP gene 3)
5370	18427	31397	0.93	3.2E-02	AW850159.1	EST_HUMAN	Saxifrage nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5652	18846	32127	1.49	3.2E-02	X68709.1	NT	IL3-CT0219-271066-022-C04 CT0219 Homo sapiens cDNA
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Stv gene
6653	19812	33200	2.4	3.2E-02	M32497.1	NT	S.griseocaneum whiG-Stv gene
6656	19815		30.61	3.2E-02	T89367.1	EST_HUMAN	Rat/polyomavirus left junction in cell line W98.14
6743	19899	33280	3.7	3.2E-02	AF173845.1	NT	yd33h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
7939	20989	34469	0.92	3.2E-02	11424049	NT	Alu repetitive element; contains LTR1 repetitive element;
8496	21577	36113	8.04	3.2E-02	6880565	NT	Sagittulus oedipus tissue kallikrein gene, complete cds
9141	22220		0.87	3.2E-02	AF106718.1	NT	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
9426	22500	36065	1.2	3.2E-02	A1278971.1	EST_HUMAN	Mus musculus kinesin family member 3c (Kif3c), mRNA
9426	22500	36066	1.2	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
10262	23287		4.51	3.2E-02	AA719795.1	EST_HUMAN	qm17b04.x1 NC1_CGAP_L105 Homo sapiens cDNA clone IMAGE:1882063 3'
10566	23601	37207	1.11	3.2E-02	U96762.1	NT	qm17b04.x1 NC1_CGAP_L105 Homo sapiens cDNA clone IMAGE:1882063 3'
							zg64b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
							gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
							Macaca mulatta chemokine receptor CCR5 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14445		1.92	3.1E-02	4503418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27559	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	8871584	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18590	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5476	18875		2.6	3.1E-02	AA278478.1	EST_HUMAN	z81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5784	18955	32259	0.77	3.1E-02	BF687742.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.58	3.1E-02	AV686088.1	EST_HUMAN	AY66038 GKC Homo sapiens cDNA clone GKCAVH09 5'
8142	22221	35764	0.48	3.1E-02	BE985092.2	EST_HUMAN	601658879R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9339	22415	35868	0.46	3.1E-02	AB72302.1	EST_HUMAN	wn57d09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36864	2.67	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14805		2.41	3.0E-02	AF187125.1	NT	Pityokleines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2652	15775	28888	1.08	3.0E-02	AA402242.1	EST_HUMAN	z85f003.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3743	16904	29908	2.82	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16938		0.93	3.0E-02	AW620223.1	EST_HUMAN	QV2-S70296-150200-040-009 ST0296 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5184	18286	31250	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5184	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.67	3.0E-02	NG9815.1	EST_HUMAN	z839a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6384	19553	32911	0.67	3.0E-02	NG9815.1	EST_HUMAN	z839a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6929	20244	33577	2.87	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M86524.1	NT	Human dystrophin gene
8317	21398		0.48	3.0E-02	BF679706.1	EST_HUMAN	602164364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286854 5'
8821	21800	35439	0.55	3.0E-02	BE512670.1	EST_HUMAN	601171626F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545047 5'
8842	21821	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-280800-108-c04 HT0704 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	22072		1.93	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37319	2.03	3.0E-02	AE001787.1	NT	Theridroma maritima section 109 of 136 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam tes244 (b)
11506	24566	38243	2.26	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11989	24974	38878	7.11	3.0E-02	AA483216.1	EST_HUMAN	ne87704.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:971263
12536	26168	31556	1.95	3.0E-02	R32019.1	EST_HUMAN	Y63304.s1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:134407 3
12943	26621		11.62	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187405 NN0038 Homo sapiens cDNA
12989	26161		4.97	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Galactose 4-epimerase beta-1, 4-galactosyltransferase mRNA, complete cds
3650	18813	28826	0.9	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30206	0.81	2.9E-02	H72805.1	EST_HUMAN	YU07010.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6421	19990	32955	6.58	2.9E-02	BF032233.1	EST_HUMAN	601452061.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5
7388	20479	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	601140728.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5
7584	20656	34133	0.65	2.9E-02	D39214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8187	21269	34793	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8187	21269	34794	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9859	22699	36482	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9859	22699	36483	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW876597.1	EST_HUMAN	EST388706 MAGC resequences, MAGN Homo sapiens cDNA
10553	23588	37198	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 777
11303	16813	28826	1.44	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002862 5
579	13771		0.76	2.8E-02	AW870163.1	EST_HUMAN	EST382234 MAGC resequences, MAGN Homo sapiens cDNA
3453	16620	29839	1.2	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3453	16620	29840	1.2	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4430	17570		0.76	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5005	18800	31866	11	2.8E-02	BE741083.1	EST_HUMAN	601594078.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3048067 5
6948	20261	33689	1.08	2.8E-02	U78860.1	EST_HUMAN	Y421008.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5
8523	21604	35142	1.67	2.8E-02	AJ005620.1	NT	Oreolaryngium plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA260762.1	EST_HUMAN	zs95508.1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:711486 5
9409	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	36144	0.76	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9674	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9674	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S9A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
1518	14671	27753	0.96	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3518	16684	29695	1.99	2.7E-02	AL161494.2	NT	
4319	17462	30447	1.93	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares_mulle, sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	y86h12.r1 Soares_mulle, sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
5362	18565	31432	0.6	2.7E-02	BF246872.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
							y33d09.r1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
5557	18755	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	T.aestivum pTTH20 mRNA for wheat type V thionin
8022	19206	32525	0.69	2.7E-02	X61670.1	NT	A.bisporus pgkA gene
6734	19880		1.02	2.7E-02	X97580.1	NT	cl66h03.s1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
7213	20078	33491	1.92	2.7E-02	AA893571.1	EST_HUMAN	lc2ag08.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8549	21690		1.36	2.7E-02	A1377036.1	EST_HUMAN	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
8818	21895	35434	0.55	2.7E-02	S43442.1	NT	Homo sapiens chromosome 21 segment HS21C082
985	13776	26796	2.62	2.6E-02	AL163282.2	NT	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
1399	14533		0.99	2.6E-02	AW650515.1	EST_HUMAN	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2439	15597	28684	2.6	2.6E-02	AA480021.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15598	28696	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	16688	28697	4.45	2.6E-02	6754241	NT	Mus musculus MHC class III region RD gene, partial cds; B1, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A, gene, partial cds; and unknown genes
2882	16158		2.07	2.6E-02	AF109906.1	NT	Chicken dorealin-1 mRNA, complete cds
6025	18154	31131	3.89	2.6E-02	L12032.1	NT	Dinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
5176	18298	31261	1.22	2.6E-02	AE002014.1	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5203	18324	31263	2.54	2.6E-02	AW241154.1	EST_HUMAN	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
8011	19195		2.94	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
8349	19518		6.85	2.6E-02	A1206030.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6555	19717	33093	2	2.6E-02	BE621748.1	EST_HUMAN	601483473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6986	20194	33619	0.83	2.6E-02	Z99064.1	NT	Vaccinia virus ORF-L, strain Wyeth

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6966	20194	33620	0.63	2.8E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33620	6.63	2.8E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20528	33989	0.65	2.8E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8703	21783	35316	0.73	2.8E-02	AA860946.1	EST_HUMAN	ak2204.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1406719 3'
9560	22702	36268	1.24	2.8E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36541	0.78	2.8E-02	AF114952.1	NT	Saccharomyces daltreensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36542	0.78	2.8E-02	AF114952.1	NT	Saccharomyces daltreensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10614	23648	37257	5.37	2.8E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747	39547	1.59	2.8E-02	AA276351.1	EST_HUMAN	z84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
11661	24949	39547	1.36	2.8E-02	AW500547.1	EST_HUMAN	U1HF-BN0-ak1-e-10-q-UJr1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12460	26150	31553	1.43	2.8E-02	BF343827.1	EST_HUMAN	602016507F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4160944 5'
12583	26392		1.32	2.8E-02	11422938	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12947	26558		1.39	2.8E-02	R43678.1	EST_HUMAN	yc6607.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element;
545	13738	26782	1.75	2.8E-02	A1783130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1557827 5'
545	13738	26783	1.76	2.8E-02	A1783130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1557827 5'
832	14010	27066	9.64	2.8E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
892	14058	27133	5.83	2.8E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950666 3'
2821	15035		2.53	2.8E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
3021	16197	29219	2.95	2.8E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	29220	2.95	2.8E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4166	18468	30302	0.92	2.8E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-e12 NN0128 Homo sapiens cDNA
4156	18468	30303	0.92	2.8E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-e12 NN0128 Homo sapiens cDNA
4322	17465	30450	4.66	2.8E-02	AW592114.1	EST_HUMAN	h38h08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5830	19021	32327	0.72	2.8E-02	A1732776.1	EST_HUMAN	z83c10.x8 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810354 3'
6322	19494		4.88	2.8E-02	BE670128.1	EST_HUMAN	7630e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element;
6338	19508		3.72	2.8E-02	BE746868.1	EST_HUMAN	601376393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6466	19633	32894	0.8	2.8E-02	L28029.1	NT	Chlamydomonas reinhardtii YSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.8E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
7843	20898	34401	1.72	2.8E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
8008	21058	34570	0.64	2.8E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8167	21249	34768	0.5	2.5E-02	BE252469.1	EST_HUMAN	601108281F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	35645	0.92	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9184	22242	35785	0.57	2.5E-02	AW025921.1	EST_HUMAN	U008c10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2616370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D.tedraum 26S ribosomal RNA, D2 domain
10810	23843	37466	0.66	2.5E-02	A1147615.1	EST_HUMAN	q62a08.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1995982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Alfa) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds;
11120	24182		2.93	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-lp
12085	25046		1.87	2.5E-02	AB007648.1	NT	Homo sapiens gene for LECT2, complete cds
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12621	25934		1.29	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12718	25476		1.83	2.5E-02	U60189.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12780	25497	32032	1.59	2.5E-02	BE973327.1	EST_HUMAN	Dicystosellum discoidium putative protein kinase MkcA (mkcA) gene, complete cds
178	13401	28431	1.44	2.4E-02	A1378582.1	EST_HUMAN	601652366R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:2070168 3'
1828	14780	27885	1.89	2.4E-02	H69894.1	EST_HUMAN	bt72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:211149 5'
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	y797f1.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17828	30609	1.69	2.4E-02	J05110.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6344	19514	32871	0.86	2.4E-02	W86680.1	EST_HUMAN	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:415791 3'
7388	20464	33928	1.11	2.4E-02	X12925.1	NT	HSAAACIKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7388	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21158		0.75	2.4E-02	AW813007.1	EST_HUMAN	Rat gene for uncoupling protein (UCP)
8128	21211		0.57	2.4E-02	M16780.1	NT	RC3-ST0186-230300-019-H05 ST0188 Homo sapiens cDNA
8636	21718		0.57	2.4E-02	H78376.1	EST_HUMAN	Human retrotransposon 3' long terminal repeat
8728	21808	35344	11.89	2.4E-02	N69442.1	EST_HUMAN	yv12c06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element
9187	22265	35806	0.75	2.4E-02	AE001125.1	NT	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284568 3' similar to gijk02909jrat3R7K Rat (rRNA) contains A3R.b1 A3R repetitive element
							Barrela burgdorferi (section 11 of 70) of the complete genome
9211	22289	35831	0.81	2.4E-02	AA625660.1	EST_HUMAN	zu91c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb.j04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	36516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (mox5) gene, complete cds
9893	22933	36517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (mox5) gene, complete cds
10011	23049	36643	2.75	2.4E-02	AF692964.1	EST_HUMAN	AY592964 GKX Homo sapiens cDNA clone GKCD5C03 5'
10186	23223	36817	2.82	2.4E-02	AA493894.1	EST_HUMAN	nt07612.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element contains element PTR5 repetitive element;
10839	23872		0.5	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3816902 5'
11874	24862	38557	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MUIS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; end unknown genes
11874	24862	38558	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MUIS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; end unknown genes
12210	25163		3.98	2.4E-02	9827903	NT	Bacteriophage BIL07, complete genome
12362	25260	32116	4.45	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12478	25330	32096	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008589.1	NT	Ctenorhynchus elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.26	2.4E-02	N42980.1	EST_HUMAN	yy08a061.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270610 5'
12883	25600	31858	1.25	2.4E-02	AA179693.1	EST_HUMAN	z013h01.1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608361 5'
1921	15064		5.25	2.3E-02	W05340.1	EST_HUMAN	z084g08.1 Soares Teta_lung_N6HL19W Homo sapiens cDNA clone IMAGE:289294 5'
1936	15079		16.26	2.3E-02	U84165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2055	15205	28321	0.99	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-250400-172-b11 UM0038 Homo sapiens cDNA
2426	15554	28681	2.88	2.3E-02	Z74293.1	EST_HUMAN	S. cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	29940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16967		0.67	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end
4267	17412	30398	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 46.6 (Cx45.6) gene, complete cds
4267	17412	30399	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30660	1.08	2.3E-02	AW699107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4571	17709	30689	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW593893.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:270671 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18469	30692	1.2	2.3E-02	AW563693.1	EST_HUMAN	xs25d08.x1 NGL CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF026487.1	EST_HUMAN	6016727279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF026487.1	EST_HUMAN	6016727279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18267	31237	0.9	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-290100-011-a07 CN0051 Homo sapiens cDNA
5266	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5266	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
8365	19535	32894	0.62	2.3E-02	BF106464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6755	19911	33306	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.69	2.3E-02	BE141475.1	EST_HUMAN	MFO-HIT0080-011099-002-c08 HIT0080 Homo sapiens cDNA
7619	20688	34164	-0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8080	21143	34661	4.52	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AL268105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AL268105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.75	2.3E-02	AL685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AL685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35967	0.84	2.3E-02	P41896	SWISSPROT	HYPOTHETICAL 55.8 KD PROTEIN B0260.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P60532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1695 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1695 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08640	SWISSPROT	GLUCOHYDROLASE
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181484 5'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181484 5'
12818	25604	31974	2.47	2.3E-02	U36394.1	NT	Streptomyces sp. alpha-1,3/4-tucosidase precursor gene, complete cds
12976	26195		1.88	2.3E-02	U11077.1	NT	Dicystostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
768	13637	26982	3.59	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1786	14936		1.79	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28329	2.17	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
3521	16887		2.03	2.2E-02	AA577765.1	EST_HUMAN	nm24e04.s1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1084782 3'
3736	16897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3856	17114	30110	0.99	2.2E-02	AW601317.1	EST_HUMAN	PM0-8T0340-1T0100-004-b03 BT0340 Homo sapiens cDNA
4029	17185	30195	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5171	18269	31262	1.37	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7398	20474	33941	3.43	2.2E-02	AV699721	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8696	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21647	35189	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22088	36630	0.92	2.2E-02	X78468.1	NT	P. vulgaris alpha tub 2 mRNA
9856	22898	36478	0.48	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9856	22898	36479	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9888	22928	36511	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.26	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12625	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
432	13627		4.48	2.1E-02	AV781502.1	EST_HUMAN	AV781502 MDS Homo sapiens cDNA clone MDSADG01 5'
462	13657		6.02	2.1E-02	AF029726.1	NT	Dicystosellum discoideum histidine kinase C (dhkc) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1418	14571	27844	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27845	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14972	28065	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28066	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28067	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28264	0.97	2.1E-02	AF190899.1	NT	Tegula auriculata major aerosol protein precursor (TUAP) mRNA, complete cds
2092	15232	28354	1.16	2.1E-02	BE072545.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2092	15232	28355	1.16	2.1E-02	BE072545.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284541 5'
3674	16837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4248	17395	30384	0.88	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4427	17587	30549	0.89	2.1E-02	BF343655.1	EST_HUMAN	602016308F1 NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4567	17705	30685	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30689	1.64	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17864	30953	5.95	2.1E-02	Y08507.1	NT	A. thaliana mitochondrial genome, part A
4852	17895	30973	0.76	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	A1823432.1	EST_HUMAN	wh54a05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5319	18432	31402	0.91	2.1E-02	BF026405.1	EST_HUMAN	60187411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.8	2.1E-02	AW379529.1	EST_HUMAN	CM4-HT0244-111195-040-n05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8716	21799	35333	0.66	2.1E-02	9760238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9703	22752	36322	0.54	2.1E-02	AA984288.1	EST_HUMAN	am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10266	23301	36899	0.75	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and
10858	23890	37508	0.49	2.1E-02	AP001519.1	NT	UmuD MucA homolog genes, complete cds; and unknown genes
11787	24777	38474	1.48	2.1E-02	6754255	NT	Bacillus halodurans genomic DNA, section 13/14
12063	25044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	am83a07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12602	18493		11.16	2.1E-02	Y19213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
12647	25615	31862	1.22	2.1E-02	L34170.1	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp90), mRNA
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	RC4-GN0050-130200-012-h04_1 GN0050 Homo sapiens cDNA
19	13257	26257	1.28	2.0E-02	BF002832.1	EST_HUMAN	Homo sapiens putative psliHbA pseudogene for hair keratin, exons 2 to 7
20	13288	26258	14.95	2.0E-02	AW895655.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
269	13488	26518	5.03	2.0E-02	6753635	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
306	13622	26556	2.95	2.0E-02	AA456538.1	EST_HUMAN	7g51c08.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13
821	14000	27054	3.63	2.0E-02	6753635	NT	MER1 repetitive element;
1111	14276	27333	0.98	2.0E-02	AL096805.1	NT	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
1226	14386	27448	0.91	2.0E-02	8922391	NT	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
							act15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
							Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [1p36.33] of Homo sapiens
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1226	14386	27449	0.91	2.0E-02	8922397	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378) mRNA
1922	15065	28108	1.84	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486) mRNA
1922	15065	28189	1.84	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486) mRNA
2859	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	28257	1.56	2.0E-02	BF002932.1	EST_HUMAN	7q51:c08.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 MER1 repetitive element;
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3298	16473		1.99	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4113	17267	30267	1.57	2.0E-02	M18096.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5219	18341		0.74	2.0E-02	AI271995.1	EST_HUMAN	q38a03.x1 NCL CGAP_K433 Homo sapiens cDNA clone IMAGE:1866076 3'
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds
7723	20787	34275	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (477)
7723	20787	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (477)
10081	23119		2.39	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10570	23605	37210	1.84	2.0E-02	AI640342.1	EST_HUMAN	wa17602.x1 NCL CGAP_K411 Homo sapiens cDNA clone IMAGE:2298315 3'
10879	23964	37592	1.65	2.0E-02	Z73988.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11683	24732	38423	1.91	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxysteroid 17 20-lyase, complete cds
11978	24983	38684	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11978	24983	38685	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18469	31535	1.8	2.0E-02	AA456538.1	EST_HUMAN	aat15b10.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12644	15973		2.28	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13188	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	y04c09.r1 Soares infant brain (NIB) Homo sapiens cDNA clone IMAGE:24875 5'
711	13993	26929	2.42	1.9E-02	AA572784.1	EST_HUMAN	nf19a07.s1 NCL CGAP_P71 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.11 L1 repetitive element;
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2970	16146	28164	9.15	1.9E-02	AA713856.1	EST_HUMAN	nw04f05.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
3078	16194	29217	1.92	1.9E-02	AV648689.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLOBLH07 3'
3332	16505		0.72	1.9E-02	AB033611.1	NT	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3699	16860		1.12	1.9E-02	N52250.1	EST_HUMAN	y228i02.s1 Soares multiple sclerosis_ZNBMHSP Homo sapiens cDNA clone IMAGE:284331 3'
3793	16954		8.1	1.9E-02	BE738088.1	EST_HUMAN	601572592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3808	16958	29871	0.83	1.9E-02	AI301183.1	EST_HUMAN	qln04c07.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30305	1.3	1.9E-02	AF141940.1	NT	Myoplasma trinitatis VihA1 precursor (VihA1) and VihA2 precursor (VihA2) genes, partial cds
4310	17453	30440	1.58	1.8E-02	P09081	SWISSPROT	HOMEOBOX BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P09081	SWISSPROT	HOMEOBOX BICOID PROTEIN (PRD-4)
4663	17708	30785	2.79	1.9E-02	AA452999.1	EST_HUMAN	446004.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Altu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18631	31609	0.96	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5808	19097	33780	0.93	1.9E-02	AB019507.1	NT	Drosophila kaneoki gene for glycerol-3-phosphate dehydrogenase, complete cds
7260	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7250	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21848	36169	1.33	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
8532	22597	36169	1.21	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9914	22554	36540	0.67	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23296	36882	1.24	1.9E-02	BF595832.1	EST_HUMAN	801862385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10458	23493	37104	0.67	1.9E-02	D64001.1	NT	Synschoecyctis sp. PCC8803 complete genome, 20/27, 2539000-2644784
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25924	31865	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis Intermediate filament gillardin mRNA, complete cds
13006	25890		1.46	1.9E-02	L11068.1	NT	Candida albicans lamBida Cas3/B fragment
358	13657	26505	1.67	1.8E-02	AW771104.1	EST_HUMAN	h15206.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
703	13896	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	601894328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1186	14348	27406	1.43	1.8E-02	X17064.1	NT	H. francisci mRNA for myelin basic protein (MBP)
1467	14621	27704	1.38	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2743	15850	28972	1.74	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 528 of the complete genome
3282	16456		0.94	1.8E-02	AI80829.1	EST_HUMAN	1652009.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080286 3'
3993	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3993	17160	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861446.1	EST_HUMAN	ak24004.st Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3'
4550	17688	30659	1.52	1.8E-02	AW636363.1	EST_HUMAN	QV4-DT0021-301299-071-311 DT0021 Homo sapiens cDNA
5068	18197	31171	2.02	1.8E-02	O80810	SWISSPROT	HYPOHETICAL PROTEIN DJB45024.2
5949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOHETICAL 7.9 KD PROTEIN IN FIXW 5 REGION
7624	20694	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7650	20694	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8663	21743	35263	0.46	1.8E-02	AW905327.1	EST_HUMAN	QV2NN1073-220400-159-R09 NN1073 Homo sapiens cDNA
8710	21790	35326	0.76	1.8E-02	6678043	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
8693	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
8693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA897543.1	EST_HUMAN	q10209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gbL11672 ZINC
10268	23303	36900	1.7	1.8E-02	BE778274.1	EST_HUMAN	FINGER PROTEIN 91 (HUMAN);
10431	23496	37072	1.29	1.8E-02	X96933.1	NT	801463545F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866963 5'
11721	23907	37530	1.76	1.8E-02	AB002337.2	NT	L. steinialis mRNA for myomodulin neuropeptide precursor
11721	23907	37531	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	38002	1.55	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11926	24912	38613	2.45	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (67)
13098	25894		1.78	1.8E-02	AF202180.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
929	14104	27187	1.34	1.7E-02	BE394869.1	EST_HUMAN	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1920	15063		2.85	1.7E-02	AL163204.2	NT	hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
2181	15316		13.13	1.7E-02	AB0004816.1	NT	hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
2705	15823		1.35	1.7E-02	7667495	NT	Homo sapiens chromosome 21 segment HS21C004
3062	16238	29289	0.99	1.7E-02	A1147615.1	EST_HUMAN	Oryctolagus cuniculus mRNA for mitogen-activated protein kinase 29, complete cds
3602	16766		4.64	1.7E-02	AW827368.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3716	16877		0.83	1.7E-02	P04929	SWISSPROT	q22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
4284	17429		1.23	1.7E-02	AA690618.1	EST_HUMAN	hF45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4317	17460		2.02	1.7E-02	R02506.1	EST_HUMAN	ac19104.s1 Stragans ovary (H937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4576	17713	30697	0.74	1.7E-02	A1305279.1	EST_HUMAN	ye8603.r1 Soares_fetal_liver_spleen_1NFSL Homo sapiens cDNA clone IMAGE:124647 5'
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	q105g07.x1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1891276 3' similar to gb.X52859 ZINC FINGER PROTEIN 30 (HUMAN);
							hF34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4836	17969	30957	1.91	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4934	18064		5.98	1.7E-02	A1015076.1	EST_HUMAN	ov51e02.s1 Soares_NSF_F8_OW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.69	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_OW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element
6709	19867	33256	1.23	1.7E-02	A1038280.1	EST_HUMAN	ov55i03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
7195	20060	33471	1.26	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34061	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7821	20972		1.71	1.7E-02	AJ010770.1	NT	Homo sapiens hyperin gene, exons 1-30
8636	21078	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9000	22940	36528	1.28	1.7E-02	AL040594.1	EST_HUMAN	DKFZp434I0314.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434I0314.5'
12063	25073	38780	1.66	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE65), mRNA
12891	26111	31667	2.35	1.7E-02	AW1903492.1	EST_HUMAN	CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA
13186	26757	31928	1.46	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.s1 NCJ_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1985287 similar to contains element MSR1 repetitive element
524	13717		4.05	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1899	14941	27626	1.37	1.6E-02	Y18899.1	NT	Treponema mallophilum flaB2, flaB3 and flid genes for flagellin subunit proteins and CAP protein homologue
2323	15455	28589	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28597	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	15754	28569	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2708	15828	28941	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCJ_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2758	15975		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29793	5.33	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160205-063-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RAGDS-like, KE2, BING4, beta 1, 3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17598	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-407 PT0012 Homo sapiens cDNA
5367	18570	31438	0.59	1.6E-02	A1281385.1	EST_HUMAN	qu42b09.x1 NCJ_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1987417 3'
5741	18934	32234	1.42	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6780	19935	33331	2.16	1.6E-02	AB015281.1	NT	Candida albicans CAGCR3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7883	20940	34446	0.96	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.8E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.8E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10246	23281		2.97	1.8E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.8E-02	AA572818.1	EST_HUMAN	nr18g03.st NCI_QGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10633	23667	37277	1.61	1.8E-02	AA572818.1	EST_HUMAN	nr18g03.st NCI_QGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11149	25968	37648	2.9	1.8E-02	Z94928.1	NT	G.gallus microsatellite DNA (LEI0260 (=T1011E11))
11488	24547	38219	2.11	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.8E-02	AJ373558.1	EST_HUMAN	yf54b10.t1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:204242 3'
12348	15455	28586	3.49	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.8E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	15343	28469	3.58	1.8E-02	N39521.1	EST_HUMAN	yv27b07.st Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:243925 3'
2244	15377	28505	1.6	1.8E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	16304	29317	1.04	1.8E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	29318	1.04	1.8E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16078	29982	1.14	1.8E-02	BF092842.1	EST_HUMAN	MR4-TN0115-080900-201-512 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.8E-02	AF260228.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19592	32957	2.07	1.8E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20547		1.69	1.8E-02	11487282	NT	Cyanophora paradoxa cyanellin, complete genome
7581	20633	34108	1.57	1.8E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34060	1.38	1.8E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8066	21147	34668	3.08	1.8E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VAR52), mRNA
9030	22109	36550	1.42	1.8E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_QGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9668	22630		0.58	1.8E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22766	36337	1.59	1.8E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36649	1.3	1.8E-02	R32667.1	EST_HUMAN	yf54b10.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.8E-02	R32667.1	EST_HUMAN	yf54b10.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10850	23983	37614	0.46	1.8E-02	T92196.1	EST_HUMAN	yv17f10.st Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.8E-02	D28547.1	NT	Rice gene for thionin h, complete cds

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCRC3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12578	25670		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0048-140100-011-c11 CN0049 Homo sapiens cDNA
430	13825		1.54	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27383	3.81	1.4E-02	7709880	NT	Homo sapiens NESH protein (LOC51225), mRNA
1295	14441		2.12	1.4E-02	U92800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1326	14483		2.49	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16459	29478	1.83	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds
3485	16653	29688	1.23	1.4E-02	AW074212.1	EST_HUMAN	X009608.X1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3573	16735	29753	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16735	29754	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	29787	0.75	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3746	16907	29911	12.14	1.4E-02	6892618	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4812	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE ressequences, MAGG Homo sapiens cDNA
4812	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE ressequences, MAGG Homo sapiens cDNA
4998	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 6'
4998	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	28210		0.74	1.4E-02	X91338.1	NT	H. sapiens LeSS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	n111c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
8333	21415		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9099	22179	35722	1.44	1.4E-02	M81702.1	NT	Candida boidini methanol oxidase (AOD1) gene, complete cds
8358	22431	35989	1.41	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22655	36227	1.66	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10780	23813		0.89	1.4E-02	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12268	25104	38358	8.95	1.4E-02	X00459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12640	25490		1.84	1.4E-02	AF324685.1	NT	Arabidopsis thaliana F21J0.2 mRNA, complete cds
12959	25625		1.45	1.4E-02	11426668	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1913	15058		1.19	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2512	15638	28769	0.98	1.3E-02	AE002445.1	NT	Nisseria meningitidis serogroup B strain MC98 section 87 of 208 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF168288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thiredoxin h, complete cds
5360	18563	31478	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5360	18563	31479	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6283	19466	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	19469	32856	1.05	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	ov06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8678	21768	35294	1.67	1.3E-02	AF156981.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23446	37051	1.88	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.96	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12845	26127		1.7	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21), from 2599451 to 2812870
12753	25499		2.56	1.3E-02	9833069	NT	Human herpesvirus 8B, complete genome
12965	25885		30.16	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
366	13676	26606	4.38	1.2E-02	AA059299.1	EST_HUMAN	z65g01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element
465	13660	26698	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3 REGION
767	13938	26983	2.87	1.2E-02	AI183522.1	EST_HUMAN	q68a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element
2246	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	15840	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	X37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15940	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	X37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16346		7.3	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stragene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:645020 5'
3369	16531	28545	2.05	1.2E-02	R62805.1	EST_HUMAN	y11508.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3362	16534	29548	0.59	1.2E-02	A1668694.1	EST_HUMAN	zb66a07.x3 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
5035	18163	31139	2.02	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
5184	18278		1.97	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5185	18317	31289	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19051	32368	1.78	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSOCR1) and wbscr6 (WBSOCR6) genes, complete cds, alternative spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150895 3'
7465	20840	34014	8.54	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
7729	20791	34280	0.66	1.2E-02	BF216650.1	EST_HUMAN	601882a09F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8166	21208	34792	2.3	1.2E-02	Q11206	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC65) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4B)
8321	21403	34929	0.56	1.2E-02	R68831.1	EST_HUMAN	y43306.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	y43306.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34994	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76987.1	EST_HUMAN	y172c08.s1 Soares fetal liver spleen NFSL Homo sapiens cDNA clone IMAGE:113774 3'
9839	22878	36461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9872	22912	36487	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12757	25988		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
12974	26634		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujware) Homo sapiens cDNA clone GEN-557 G08 5'
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	zm65a11.s1 Stragene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:630924 3'
1743	14852	27986	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1743	14852	27987	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2096	15236	28357	5.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2942	16119		5.31	1.1E-02	N99523.1	EST_HUMAN	z44005.t1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	20792	3.59	1.1E-02	AI853508.1	EST_HUMAN	IQ953.10.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW.XPF_HUMAN
4222	17370		0.66	1.1E-02	AW813798.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4981	18081	31057	1.27	1.1E-02	AL048393.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
6277	19451	32800	0.89	1.1E-02	U66480.1	NT	DKFZp586E0924_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
7773	20830	34321	2.19	1.1E-02	BE149611.1	EST_HUMAN	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylanase
7999	21039	34551	1.25	1.1E-02	9631294	NT	RC1-H10258-100300-018-h07 HT0258 Homo sapiens cDNA
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	Melanoplus sanguinipes entomopoxvirus, complete genome
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21820	35458	0.69	1.1E-02	AW996160.1	EST_HUMAN	METALLOTHIONEIN (MT-1/MT-2)
9022	22101	35641	0.7	1.1E-02	C04803.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0046 Homo sapiens cDNA
9103	22182	35727	7.44	1.1E-02	Q61982	SWISSPROT	CC4803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10299	23334	36939	4.06	1.1E-02	AA314966.1	EST_HUMAN	zn24e01.t1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
11224	24203	37934	2.41	1.1E-02	11435505	NT	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
12195	25152		4.01	1.1E-02	AA669239.1	EST_HUMAN	Homo sapiens T-box 5 (TBX5), mRNA
7	13245	26247	8.82	1.0E-02	AW846120.1	EST_HUMAN	ab77111.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
1552	14705	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	Alu repetitive element
2938	15761		1.71	1.0E-02	AA805389.1	EST_HUMAN	MR3-CT0176-111098-003-e10 CT0176 Homo sapiens cDNA
3159	16334	29344	2.88	1.0E-02	BE835556.1	EST_HUMAN	CM2-HT0177-041089-017-h12 HT0177 Homo sapiens cDNA
3336	16509	29525	1.24	1.0E-02	BE969999.1	EST_HUMAN	cc22h08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3598	16762		0.7	1.0E-02	AW845921.1	EST_HUMAN	RCQ-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3986	17143	30148	0.85	1.0E-02	AI050893.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
4002	17159	30165	0.59	1.0E-02	AL163302.2	EST_HUMAN	MRO-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4899	18029	31017	5	1.0E-02	AL163302.2	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4999	18098	31074	4.14	1.0E-02	R95597.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
5116	18243	31208	0.83	1.0E-02	AL161593.2	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5242	18364	31332	1.96	1.0E-02	P06599	SWISSPROT	y954h01.t1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:199633 5'
5532	18729	31745	0.81	1.0E-02	H52881.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
							EXTENSIN PRECURSOR
							y936h11.t1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5886	19055	32382	0.66	1.0E-02	AF30388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.29	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syty2) gene, complete cds
6310	19482	32838	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01.BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01.BT0356 Homo sapiens cDNA
6901	20216	33948	1.69	1.0E-02	Z29642.1	NT	Z.mays U3snRNA pseudogene
8589	22848	36219	6.34	1.0E-02	BF036331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9593	22848	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Cytrichia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11573	24628		1.7	1.0E-02	AF1417981.1	EST_HUMAN	ig55h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1
11649	24728	38420	1.85	1.0E-02	AV760016.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 80-ALPHA (HUMAN); contains Alu repetitive element; contains element MER6
12278	26206		1.76	1.0E-02	Q62203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12339	25841	31762	3.58	1.0E-02	AW235521.1	EST_HUMAN	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12366	26002		4.31	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02.DT0007 Homo sapiens cDNA
12764	25974		1.4	1.0E-02	AIJ27605.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12949	26060		2.91	1.0E-02	XG2654.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
916	14001	27156	5.69	9.0E-03	AI798126.1	EST_HUMAN	H.sapiens gene for Mx491/CD83 antigen
1293	14449		1.66	9.0E-03	BE781889.1	EST_HUMAN	wh4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2489	15596	28721	2.64	9.0E-03	AL161559.2	NT	MER22 MER22 repetitive element.
2971	16147	29165	0.81	9.0E-03	AI251744.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
3768	16919	29921	0.66	9.0E-03	J05184.1	NT	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5931	19117		1.19	9.0E-03	AI809792.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
6789	19922		4.01	9.0E-03	BE746088.1	EST_HUMAN	Saccharomyces cerevisiae thermopsin gene, complete cds
7823	20893	34169	0.61	9.0E-03	AI242219.1	EST_HUMAN	wf7704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
7840	20708	34188	0.61	9.0E-03	8922570	NT	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
8059	21142		0.8	9.0E-03	AL039991.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
8443	21524		0.54	9.0E-03	AF223391.1	NT	Homo sapiens hypothetical protein FLJ10850 (FLJ10850), mRNA
10050	23098	36690	0.54	9.0E-03	P28011	SWISSPROT	DKFZp434L0412.1 t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
10068	23104	36707	1.47	9.0E-03	P28008	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
							COLLAGEN ALPHA (V) CHAIN PRECURSOR

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.88	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11951	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw71609.x1 NCL CGAP_L224 Homo sapiens cDNA clone IMAGE:3183161.3
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	z130ec3.1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598.3 similar to contains
1013	14185	27248	12.89	8.0E-03	AF108658.1	NT	Alu repetitive element
2228	15360	28489	1.87	8.0E-03	AL163283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2817	15741	28853	3.05	8.0E-03	P10286	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3442	16610	29628	1.02	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3766	16927	29930	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3766	16927	29931	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4502	17842	30627	6.73	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300800-223-b05 NN0119 Homo sapiens cDNA
4839	17872	30961	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4839	17872	30962	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18390	31358	0.94	8.0E-03	AJ140251.1	EST_HUMAN	AJ140261 PLACE2 Homo sapiens cDNA clone PLAGE2000223.5
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, Iapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds, Sacm21 gene, partial>
6328	25823	32557	1.27	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
6899	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7059	20112		1.06	8.0E-03	V01108.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7357	20436		1.43	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
7714	20778		1.8	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9111	22190	35734	3.53	8.0E-03	AW808692.1	EST_HUMAN	MP1-ST0111-111192-011-H06 ST0111 Homo sapiens cDNA
9180	22258	35801	0.68	8.0E-03	9789866	NT	Mus musculus fusion 2 (human) (Fus2), mRNA
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0877-040400-131-g03 BT0877 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE768441.1	EST_HUMAN	601475519F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3878405 5'
11237	24300		2.79	8.0E-03	Z49552.1	NT	S. cerevisiae chromosome X reading frame ORF YJRT152w
11663	24742	38433	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
11863	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
12015	24898	38701	4.37	8.0E-03	AF064599.1	NT	Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds
12205	25159		1.89	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12252	25181		7.14	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.16	8.0E-03	AI277808.1	EST_HUMAN	qm55c08.x1 Soares_placenta_81c9weeks_2NtHP81c0W Homo sapiens cDNA clone IMAGE:1892752 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
986	14170	27231	3.28	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27361	3.55	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/TFH TRANSSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1426	14590	27653	3.39	7.0E-03	AA668288.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFH-2)
1532	14655	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	eb79b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2332	16090	28598	2	7.0E-03	P04929	SWISSPROT	xx21502.x1 Soares_NFL_T_QBEC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2695	15815		0.98	7.0E-03	AWJ72132.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3648	16811	29824	0.65	7.0E-03	AI150273.1	EST_HUMAN	hm07h07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element
3663	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	q34k02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3914	17073	30071	1.13	7.0E-03	AF198344.1	NT	U1-H-Big-akb-q-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733661 3'
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4721	17856		0.99	7.0E-03	AW630888.1	EST_HUMAN	U1-H-Big-akb-q-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733661 3'
5103	18231		6.54	7.0E-03	AL163278.2	NT	hm89a05.y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2869935 5'
5940	18126		0.72	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6238	25821		4.42	7.0E-03	AW861059.1	EST_HUMAN	yf82g01.r1 Soares_fetal_liver_spleen_TNFS_Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN)
8444	19611	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
9667	18826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	z633101.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6696	19853	33243	1.05	7.0E-03	BE857385.1	EST_HUMAN	7q34b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.2 TAR1 repetitive element ;
7689	20754	34238	4.76	7.0E-03	Z35838.1	NT	GM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7689	20754	34238	4.76	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34632	0.59	7.0E-03	AJ228043.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34633	0.59	7.0E-03	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21384	34905	2.48	7.0E-03	BE175667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8813	21892	35433	0.68	7.0E-03	AF281074.1	NT	RC9-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9597	22852		0.64	7.0E-03	AF111188.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
9794	22834	35414	0.68	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine pathobyl transferase, subunit II gene, complete cds; and unknown genes
9921	22861	36548	2.72	7.0E-03	P48982	SWISSPROT	y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246008 3' similar to contains
9921	22861	36549	2.72	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10513	23348		1.34	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10704	23737		0.82	7.0E-03	AI798734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10800	23833	37456	0.47	7.0E-03	BE154643.1	EST_HUMAN	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	wc37609 x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	PM3-HT0344-181169-002-g06 HT0344 Homo sapiens cDNA
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
12792	26189		1.95	7.0E-03	H94055.1	EST_HUMAN	Homo sapiens partial MUC8B gene, exon 1-29
12800	25834		1.46	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC8B gene, exon 1-29
12908	25601		1.76	7.0E-03	Y17455.1	NT	yv15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
13098	28186		1.68	7.0E-03	AL163300.2	NT	Alu repetitive element;
1299	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 6'
1299	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
2831	16045	26054	0.94	6.0E-03	AF112374.1	NT	Homo sapiens chromosome 21 segment HS21C100
2956	16133	29147	3.29	6.0E-03	AA759135.1	EST_HUMAN	SW:PXK_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2956	16133	29148	3.29	6.0E-03	AA759135.1	EST_HUMAN	h22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
3318	16491		2.27	6.0E-03	HT5690.1	EST_HUMAN	SW:PXK_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
							Danio rerio odorant receptor gene cluster
							ah78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							y17h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF180338.1	NT	Natolcus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	16636	29655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isolectin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3469	16636	29655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isolectin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3636	16800		1.11	6.0E-03	W37985.1	EST_HUMAN	zot13a17.1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3750	16911	29914	3.73	6.0E-03	BF510886.1	EST_HUMAN	U14-B14-epm-c-08-Q-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17038	30034	1.31	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl) mRNA
4032	17188	30189	0.8	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240989-021-b10 CT0204 Homo sapiens cDNA
4087	17223		1.26	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4484	17624		1.54	6.0E-03	AI016833.1	EST_HUMAN	ov33c11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17650	30535	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5305	18422	31392	0.8	6.0E-03	AA88072.1	EST_HUMAN	ag5509.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404266 3'
5281	25822	32903	0.68	6.0E-03	9627521	NT	Varicella virus, complete genome
5956	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
5994	18513	31505	0.87	6.0E-03	BE283748.1	EST_HUMAN	80111233F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7399	20477	33944	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7824	20878	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds containing MER10.b1 MER10 repetitive element
8042	21125	34846	6.71	6.0E-03	AI033980.1	EST_HUMAN	gw13a04.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to
8181	21243	34763	2.76	6.0E-03	AW799337.1	EST_HUMAN	RCO-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8236	21318		1.65	6.0E-03	BF038188.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
9754	22892	36262	7.03	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	AI432661.1	EST_HUMAN	922c02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AI011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A
10503	23538		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fnd gene
10515	23649	37258	0.64	6.0E-03	X69368.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10661	23695		0.54	6.0E-03	AF245505.1	NT	M thermophilum complete plasmid pV1 DNA
10683	24062	37687	1.56	6.0E-03	AW962184.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
11049	24126		1.94	6.0E-03	11345814	NT	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
							Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37838	2.86	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	25598		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	25926		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450298 (section 39 of 148) of the complete genome
12532	25993		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	25957		1.63	6.0E-03	Q82209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SOP-1 PROTEIN)
12944	26622		2.41	6.0E-03	AJ245480.1	NT	Brassica napus s10 gene for S-locus glycoprotein, cultivar T2
13095	26018		1.81	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
13147	25746		1.19	6.0E-03	BF110298.1	EST_HUMAN	7635617.1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1136	14301	27357	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1601	14754		1.08	5.0E-03	AI138977.1	EST_HUMAN	q079005.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2746	15863	28974	2.43	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	29392	3.87	5.0E-03	T87623.1	EST_HUMAN	yc81709.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y86602.s1 Soares breast 2N1bHstHomo sapiens cDNA clone IMAGE:155666 3'
3351	16523		0.84	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3790	16951	29957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3854	17014	30014	0.81	5.0E-03	U36914.1	EST_HUMAN	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.84	5.0E-03	AA299875.1	NT	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.65	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4421	17562	30546	0.71	5.0E-03	H78355.1	EST_HUMAN	y07910.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:240068 5'
4423	17014	30014	0.78	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17866	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SOL gene locus

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30864	1.56	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5286	18405		1.9	5.0E-03	4768747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE θ , Y CHROMOSOME)
6169	19346	32691	2.82	5.0E-03	000507	SWISSPROT	CHROMOSOME
6204	19379		0.88	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AR39, section 82 of 84 of the complete genome
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	605444564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6986	18606	31520	7.22	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7237	20321	33765	0.61	5.0E-03	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#933206) Homo sapiens cDNA clone HFBOR93 similar to EST containing Alu repeat
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031098-011-07 CT0255 Homo sapiens cDNA
7944	20994	34505	7.18	5.0E-03	AB018816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8415	21496	35027	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8415	21496	35028	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8433	21514	35045	1.99	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8811	21880		5.83	5.0E-03	M91132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9007	22088	35629	1.21	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9140	22219	35763	0.52	5.0E-03	M25080.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10044	23082	36884	1.03	5.0E-03	L21710.1	NT	Pisum sativum berghel 58 kDa phosphoprotein mRNA, partial cds
10176	23213	36805	0.74	5.0E-03	AW821886.1	EST_HUMAN	RCO-ST0379-210100-032-02 ST0379 Homo sapiens cDNA
10360	23395	37006	0.66	5.0E-03	AA533143.1	EST_HUMAN	h48ht0.st NCI CGAP_P99 Homo sapiens cDNA clone IMAGE:995587
10539	23574	37181	0.47	5.0E-03	7682667	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10608	23729		0.47	5.0E-03	AA553281.1	EST_HUMAN	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126290 3'
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	kn56g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	kn56g05.x1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.12 L1 repetitive element
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	jb09ed04.r1 Stratagene placenta (#937226) Homo sapiens cDNA clone IMAGE:70686 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11615	24666		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12070	25051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	25051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.86	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Scores ovary tumor NIH/OT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
12802	25935		5.99	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
13002	25951	31951	2.66	5.0E-03	AW449109.1	EST_HUMAN	UI-H-B13-akf-f08-Q-UJ.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734215 3'
2422	13484	26483	1.54	4.0E-03	AW500166.1	EST_HUMAN	UI-HF-BN0-akc-h-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
331	13545	26575	1.75	4.0E-03	R45482.1	EST_HUMAN	ys51e04.s1 Scores infant brain T1B1B Homo sapiens cDNA clone IMAGE:35988 3'
456	13651	26689	1.36	4.0E-03	P54875	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
616	13805	26825	4.37	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	ys51e04.s1 Scores infant brain T1B1B Homo sapiens cDNA clone IMAGE:35988 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1174	14337	27393	34.06	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1196	14368	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1331	14486	27555	1.48	4.0E-03	AA284374.1	EST_HUMAN	zs59e01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1783	14932	28026	2.68	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and oligodendrocyte associated protein A T1-46 mRNA, complete cds
2076	15215	28334	17.33	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2321	15453		2.06	4.0E-03	BE410558.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2352	15483	28616	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15762	28875	1.95	4.0E-03	U52111.2	NT	
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	
2755	15872	28980	2.97	4.0E-03	AJ277365.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28981	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15977	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3297	16471	29491	1.09	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							PM1-HT0340-151289-003-108 HT0340 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3297	18471	29492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-008 HT0340 Homo sapiens cDNA
3619	18783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X8804.1 NCL CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3619	18783	29799	0.83	4.0E-03	AW188426.1	EST_HUMAN	X8804.1 NCL CGAP Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3714	18875	29890	0.84	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 511 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
4021	18875	29880	0.85	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 511 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17199	30207	0.72	4.0E-03	AF060888.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4102	17259		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
5339	18452	31420	0.98	4.0E-03	AW50547.1	EST_HUMAN	UHF-BNO-wk-e-10-0-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
5390	18592	31584	1.59	4.0E-03	AF005859.1	NT	Drosophila melanogaster arn2D7 (arn2D7) mRNA, complete cds
5815	18713	31728	27.24	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32419	3.1	4.0E-03	P04198	SWISSPROT	(HPRC)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.J1 T61 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.87	4.0E-03	AW590572.1	EST_HUMAN	ig46c07.x1 NCL CGAP G08 Homo sapiens cDNA clone IMAGE:2948652 3'
8439	19808	32989	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
8609	19963	33387	1.07	4.0E-03	AA813222.1	EST_HUMAN	q32111.at Soares_Iaalis_NHT Homo sapiens cDNA clone 1392045 3'
8914	20229	33692	1.41	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33498	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33889	3.73	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20680	34136	0.95	4.0E-03	AI681483.1	EST_HUMAN	h37g12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20682	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7631b02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20759		0.85	4.0E-03	X92109.1	NT	H.sapiens hcpIX gene
8128	21210	34731					ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8338	21320	34838	0.57	4.0E-03	Q9T192	SWISSPROT	(ADAM-TS6) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8398	21479	35008	4.81	4.0E-03	AF111944.1	NT	Dasyatis leucon discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8695	21745	35284	2	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8761	21840	35381	0.87	4.0E-03	AF139827.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
			0.51	4.0E-03	Y12855.1	NT	Homo sapiens P2X7 gene, exon 12 and 13
8911	21880	35529					h48b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9090	22169		7.05	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.24	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
			3.76	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9825	22865	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22865	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23169	36766	0.83	4.0E-03	H30664.1	EST_HUMAN	yp42g12.r1 Soares retina N2b3HR Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37229	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37886	1.35	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
12072	25053	38782	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		6.84	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028096 5'
12541	25357		1.95	4.0E-03	AW604278.1	EST_HUMAN	UIHF-BN0-ep-g-040-JL11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12858	26053		2.18	4.0E-03	AW614598.1	EST_HUMAN	hH02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
12871	25681		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
382	13690	28826	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
802	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14846	27630	3.66	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2367	15488		6.37	3.0E-03	Z32621.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2368	15499	28624	1.14	3.0E-03	U46958.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15499	28625	1.14	3.0E-03	U46958.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3056	16232		0.77	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rpoM1 gene
3152	16327	28338	3.55	3.0E-03	BE379298.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609633 5'
3220	16394	29405	2.63	3.0E-03	AW802687.1	EST_HUMAN	IL2-JN10076-240300-056-D03 UMB076 Homo sapiens cDNA
3504	16871	29681	2.16	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3513	16679		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17289	30291	1.67	3.0E-03	AJ762278.1	EST_HUMAN	af04f09.y6 Gaessler Wilm's tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4641	17777	30759	4.62	3.0E-03	AJ536141.1	EST_HUMAN	xs8.P10.H3 conorm Homo sapiens cDNA 3'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4858	17991	30978	0.89	3.0E-03	AL119087.1	EST_HUMAN	DKFZp761B0712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712.5'
4855	18085	31061	2.06	3.0E-03	AI732754.1	EST_HUMAN	ab18a05.x6 Stragene lung (H837210) Homo sapiens cDNA clone IMAGE:841142.3' similar to contains Alu repetitive element
4978	18107	31063	5.53	3.0E-03	BE787946.1	EST_HUMAN	601482716F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3685483.5'
5255	18375	31341	0.9	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAT1) mRNA
5255	18375	31342	0.9	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAT1) mRNA
5262	18381	31347	1.75	3.0E-03	AI193860.1	EST_HUMAN	q88b10.x1 Soares_fetal_lung_NHL-19W Homo sapiens cDNA clone IMAGE:1745275.3' similar to SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17 ;contains MSR1.12 MER22 repetitive element
5380	18582	31451	3.36	3.0E-03	8922498	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539). mRNA
5673	18867	32153	1.09	3.0E-03	AJ248981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U93323.1	NT	Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	aat310.r1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:813163.5'
7168	20301	33744	0.75	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7354	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pep33 gene for purine-cytosine permease
7891	20756	34241	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8124	21206	34726	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8360	21431	34955	1.4	3.0E-03	N92590.1	EST_HUMAN	2b27b04.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:304783.3'
8490	21571	35108	0.47	3.0E-03	AI860028.1	EST_HUMAN	w124d09.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425841.3'
8510	21591		0.63	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35276	1.34	3.0E-03	P51089	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8678	21789	35296	1.5	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8788	21865		1.45	3.0E-03	Q8QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9192	22270		10.8	3.0E-03	AW613774.1	EST_HUMAN	h180f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131.3' similar to contains L1.11 L1 repetitive element
9245	22322	35866	4.26	3.0E-03	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9269	22345	35896	0.66	3.0E-03	AI016731.1	EST_HUMAN	o03d12.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1638247.3' similar to gb:57138_mai
9280	22356	35906	0.53	3.0E-03	BF33078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9609	22684		0.78	3.0E-03	D80901.1	NT	602055980F1 NCL_CGAP_Bm94 Homo sapiens cDNA clone IMAGE:4183938.5'
9646	21089	34604	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9836	22676		0.56	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071289-003-d07 HT0344 Homo sapiens cDNA POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9808	22948		6.51	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
10099	23137	36738	2.31	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23378	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11085	24159		2.67	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24782	38457	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24782	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24638	38532	1.36	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
12077	25057		1.46	3.0E-03	AW1294812.1	EST_HUMAN	U1-H-B12-ah1-d06-Q-UJ st NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
12199	26948		1.62	3.0E-03	AI525056.1	EST_HUMAN	parrina-5.E07.7 btkmur Homo sapiens cDNA 5'
12235	25179	38346	1.24	3.0E-03	AA993164.1	EST_HUMAN	contains L1.13 MER26 repetitive element ;
12296	26050		1.78	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydrolase, partial cds
12481	25333	32057	1.23	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	Y115h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1394	14548	27624	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1397	14551	27626	1.42	2.0E-03	AA661805.1	EST_HUMAN	nu8601.s1 NCI CGAP Alvi Homo sapiens cDNA clone IMAGE:1217593
1406	14660	27634	20.85	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14698	27777	2.26	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA460138.1	EST_HUMAN	Zx42a10.r1 Soares fetal liver NB2HF8, 8w Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.09	2.0E-03	BE144908.1	EST_HUMAN	OM2-HT0183-061089-018-403 HT0183 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15498	29588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2647	15770		4.93	2.0E-03	AI137782.1	EST_HUMAN	U1H-B11-adj-g-10-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16870	29680	4.92	2.0E-03	AA413782.1	EST_HUMAN	x242a10.r1 Soares_t04.fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3510	16876	29686	0.96	2.0E-03	BF568955.1	EST_HUMAN	602183600T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3759	16917	29519	5.48	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4062	17218	30228	0.82	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17376	30364	2.39	2.0E-03	P30374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP82; COAT PROTEIN GP36]
4290	17435	30423	1.02	2.0E-03	AA179693.1	EST_HUMAN	2013K01.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
4336	17479		13.93	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17670		1.99	2.0E-03	L35078.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4547	17685	30670	1.22	2.0E-03	AW297380.1	EST_HUMAN	U1H-BW0-adj-g-0-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17689	30780	2.11	2.0E-03	A1064748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17803	30781	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17961	30649	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	yx45e02.s1 Soares adult brain N2b4Hb65Y Homo sapiens cDNA clone IMAGE:180890 3'
4962	18061	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18768	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	25810	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0993 protein, partial cds
5828	19019	32265	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xellin1 mRNA, complete cds
6236	19411	32758	3.93	2.0E-03	P23477	SWISSPROT	A1P-DEPENDENT NUCLEASE SUBUNIT B
6236	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	A1P-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6476	19643	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6478	19645	33007	7.66	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19679	33049	2.16	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19680	33050	0.76	2.0E-03	U709075.1	EST_HUMAN	A7709075 ADC Homo sapiens cDNA clone ADCAEF09 6'
6547	19708	33082	1.45	2.0E-03	X04451.1	NT	L1-actulium mRNA for lxy4-RNA synthetase (LVERS)

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6736	19892		1.36	2.0E-03	AB091089.1	EST_HUMAN	wu39109.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element ;
6775	19830	33326	0.7	2.0E-03	AA677631.1	EST_HUMAN	2f73a17.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7098	18625	31517	1.35	2.0E-03	AB038502.1	NT	Ceanorhabditis elegans mRNA for galeciclin LEC-11, complete cds
7231	20136	33654	3.3	2.0E-03	BE057896.1	EST_HUMAN	CM4-BT0366-061299-054-d01 BT0366 Homo sapiens cDNA
7294	20376	33833	0.65	2.0E-03	AZ28883.1	EST_HUMAN	qm6ad11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:186685 3'
7444	20521	33994	0.8	2.0E-03	T86569.1	EST_HUMAN	yt77g10.r1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:114306 5'
7794	20650	34342	1.41	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	h37606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY. ;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8459	21540	35069	0.84	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C6G9.05 IN CHROMOSOME 1
8481	21562	35097	1.09	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8536	21617	35153	1.04	2.0E-03	6005655 NT		Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8536	21617	35164	1.04	2.0E-03	6005655 NT		Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone IMAGE:1004839 5'
8614	21694		0.9	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9396	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9396	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9441	22515	36079	1.07	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9726	22791	36362	0.71	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:194286 3'
9726	22791	36363	0.71	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:194286 3'
9756	22896	36284	3.33	2.0E-03	P24921	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9868	22908	36493	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36494	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9924	22964	36552	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9024	22934	36553	0.6	2.0E-03	AF097732.1	NT	Homo sapiens catenase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	36765	0.96	2.0E-03	AW884269.1	EST_HUMAN	QV8-OT0064-060400-144-401 OT0064 Homo sapiens cDNA
10248	23283		6.26	2.0E-03	AA257376.1	EST_HUMAN	Z810606.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:884764 3'
10328	23692	37270	0.46	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140900-001-e05 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	MB6524.1	NT	Human dystrophin gene
11778	20650	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330909.1	EST_HUMAN	RCS-BT0333-310800-115-404 BT0333 Homo sapiens cDNA
11844	24833	38528	9.84	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12160	25140		3.37	2.0E-03	AI625745.1	EST_HUMAN	ly65103.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12168	25155	38833	4.31	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G :
12222	25171	38836	1.71	2.0E-03	AI084325.1	EST_HUMAN	Homo sapiens SEL1L (SEL1L) gene, partial cds
12245	18497		4.88	2.0E-03	AJ246167.1	NT	cy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
12462	26140		4	2.0E-03	AV697866.1	EST_HUMAN	TR:P87535 P87535 PS-PLA1 PRECURSOR. ;
12661	26383	32039	1.29	2.0E-03	Y00508.1	NT	Camelus dromedarius cvrp19 gene for Immunoglobulin heavy chain variable region
							AV697868 GKC Homo sapiens cDNA clone GKGGX005 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b,
13060	25927		2.46	2.0E-03	AV697866.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
452	13648	26684	1.38	1.0E-03	H93471.1	EST_HUMAN	AV697866 GKC Homo sapiens cDNA clone GKGGX005 5'
							y88c08.t1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
852	14029	27091	1.55	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barleed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
							Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
852	14029	27092	1.55	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barleed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1119	14284	27339	2.61	1.0E-03	AI865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1139	14304	27360	1.61	1.0E-03	AI854572.1	EST_HUMAN	wk86g08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422268 3'
							wk83a10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1192	14354	27412	0.85	1.0E-03	AI692616.1	EST_HUMAN	w486a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu
							repetitive element;
2084	16224	26346	3.42	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMM/Mi)
2222	15356	26486	9.52	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3044	16220	26241	1.37	1.0E-03	AB03117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED
3280	16434	26451	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3290	18434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3374	18548	29560	0.75	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16796	20813	0.94	1.0E-03	U88061.1	NT	Human MUC2 gene, promoter region
3632	16796	29814	0.94	1.0E-03	U88061.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4034	17160	30200	0.98	1.0E-03	AW170552.1	EST_HUMAN	h63d07.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.11 TAR1 repetitive element;
4044	17200	30211	0.91	1.0E-03	Z49649.1	NT	S. cerevisiae chromosome X reading frame ORF YJR149w
4566	17694	30673	2.34	1.0E-03	BE938162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4598	17735	30715	4.89	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBA9909
4765	17920	30808	0.81	1.0E-03	U28449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31050	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4945	18075	31051	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4946	18076	31276	6	1.0E-03	BE164067.1	EST_HUMAN	PMO-HT0339-200400-070-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O46409	SWISSPROT	AFOLIPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	nv5102.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176955 3'
5423	18624	31600	2	1.0E-03	AA290951.1	EST_HUMAN	zs4401.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5572	18768	31809	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5690	18884	32176	0.95	1.0E-03	BE796491.1	EST_HUMAN	801598841FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943654 5'
5696	18890	32181	1.77	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
6033	19216		0.59	1.0E-03	BF541639.1	EST_HUMAN	80208042F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4068907 5'
6144	19322		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6184	19360	32708	0.85	1.0E-03	BE938393.2	EST_HUMAN	601657519R1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3875603 3'
6321	19493		8.77	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19631	32992	1.11	1.0E-03	T87761.1	EST_HUMAN	yc03a11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5'
6539	19702		1.88	1.0E-03	AW902595.1	EST_HUMAN	QY3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6898	20046	33485	1.41	1.0E-03	L77570.1	NT	Homo sapiens D1George syndrome critical region, centromeric end
7302	20384	33843	2.81	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7658	20724		1.12	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7817	20872	34370					Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7885	20937	34443	1.98	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7934	20984	34492	3.44	1.0E-03	M63376.1	NT	601491081F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3893276 5'
8073	21155	34674	0.79	1.0E-03	BE880044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8136	21218	34739	0.68	1.0E-03	AF274581.1	NT	Homo sapiens partial stein-1 gene
8337	21418	34941	5.02	1.0E-03	AJ251973.1	NT	zkg7d09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element ;
8438	21519	35048	1.95	1.0E-03	AA122270.1	EST_HUMAN	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8825	21705	35241	2.36	1.0E-03	AF153980.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9144	22223		0.75	1.0E-03	U28397.1	NT	V carter gene encoding vdxoxapsh
9170	22248	35791	1.48	1.0E-03	Y11204.1	NT	CMS-LT0078-170200-092-407 LT0079 Homo sapiens cDNA
9281	22357		0.65	1.0E-03	AW840353.1	EST_HUMAN	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9319	22395	35947	0.65	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) cbl subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cbl subunit mRNA, complete cds
9798	22838		3.89	1.0E-03	M30471.1	NT	qf58d01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848573 3' similar to
9807	22847	36424	0.47	1.0E-03	AJ247482.1	EST_HUMAN	gskM97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermoboga neapolitana alpha-1,6-galactosidase (agA) gene, complete cds
10025	23063	36660	2.06	1.0E-03	AF011400.1	NT	Thermoboga neapolitana alpha-1,6-galactosidase (agA) gene, complete cds
10366	23401	37012	2.08	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE
10372	23407		0.88	1.0E-03	AF003528.1	NT	PROTEOGLYCAN II (DSPG)
10522	23557	37165	9.37	1.0E-03	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10823	23856	37478	0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10823	23856	37478	1.08	1.0E-03	AJ024950.1	EST_HUMAN	ov79108.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643176 3' similar to contains MER39, b1
10823	23856	37478	0.5	1.0E-03	AE004782.1	NT	MER39 MER39 repetitive element ;
10823	23856	37478	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PA01, section 323 of 528 of the complete genome
10823	23856	37478	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PA01, section 323 of 528 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10830	23863		0.53	1.0E-03	AA706202.1	EST_HUMAN	ag83f12.s1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element;
10802	23866	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181088-011-a09 CT0279 Homo sapiens cDNA
10802	23866	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181088-011-a09 CT0279 Homo sapiens cDNA
10889	24068	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TR:Q26195 Q26195 PVA1 GENE.;
11425	24486		2.63	1.0E-03	AI759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF-11 5'
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11898	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11924	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-BINDING ACTIVITY)
11924	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-BINDING ACTIVITY)
12176	25136	38831	5.51	1.0E-03	BE894488.1	EST_HUMAN	(TRANSCRIPTION FACTOR NTF-1)
12679	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872035 5'
12899	25590		1.17	1.0E-03	11465834	NT	Nicotiana tabacum chloroplast, complete genome
5327	18440	31409	0.7	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5739	18969		2.09	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6388	19557		0.56	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6615	19775	33166	1.27	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9843	22883		1.46	9.0E-04	AB037203.1	NT	Glycylthiza glabra GpbAS1 mRNA for beta-amylin synthase, complete cds
1517	14670		1.07	8.0E-04	X96469.1	NT	X. laevis mRNA for C4SR protein
4298	17439		4.4	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4887	18017	31002	2.5	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11412	24473		2.59	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11576	24631		1.87	8.0E-04	AI571099.1	EST_HUMAN	b85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1874	15018	28127	1.11	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2472	15599	28724	1.45	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2778	15894	28004	1.33	7.0E-04	AL169210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3353	16526	28540	1.4	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6221	19396	32745	0.93	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.st NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.03 L1 L1
6642	19801		2.33	7.0E-04	AI769331.1	EST_HUMAN	repetitive element:
7376	20455		0.72	7.0E-04	AK024446.1	NT	wg36f09.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24863		1.7	7.0E-04	U78027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11893	24881	38578	3.78	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Bruton's tyrosine Kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12723	25481		9.28	7.0E-04	BE077941.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
13001	25650		2.68	7.0E-04	R17336.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
13038	25692		5.43	7.0E-04	8005655	NT	yj13c06.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
2760	15876		0.97	6.0E-04	BF341380.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
4069	17225	30232	1.64	6.0E-04	AI862525.1	EST_HUMAN	002013339F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149287 5'
4201	17350	30341	0.65	6.0E-04	K01315.1	NT	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4201	17350	30342	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30430	3.91	6.0E-04	U15983.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4565	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4565	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
8050	21133		4.58	6.0E-04	P46408	SWISSPROT	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
8205	21287		0.51	6.0E-04	H92947.1	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
10185	23222		3.26	6.0E-04	AL048507.2	EST_HUMAN	y64a011.st Scores pineal_gland_N3HPO Homo sapiens cDNA clone IMAGE:231856 3' similar to contains LOR1 repetitive element:
10215	23251		0.53	6.0E-04	AI859286.1	EST_HUMAN	DKFZ568M2024_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp568M2024
10285	23320	36922	2.29	6.0E-04	BE005880.1	EST_HUMAN	w135g02.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2428830 3'
10547	23582		0.84	6.0E-04	AF287478.1	NT	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
11774	24766	38462	2.07	6.0E-04	AJ229042.1	NT	Lytechinus variegatus embryonic blastocoelear extracellular matrix protein precursor (ECM3) mRNA, complete cds
11866	24864	38540	2.47	6.0E-04	AW013847.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11937	24923		1.62	6.0E-04	Q01768	SWISSPROT	UHH-B10-aab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
12363	26007		3.31	6.0E-04	AW380619.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
13228	25797		14.14	6.0E-04	AB17068.1	EST_HUMAN	RC1-HT0269-261188-012-008 HT0269 Homo sapiens cDNA
668	13854	26882	7.98	5.0E-04	OT0341	SWISSPROT	RC1-HT0269-261188-012-008 HT0269 Homo sapiens cDNA
							wj7fg11.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element:
							HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1831	14684		2.03	5.0E-04	AW851844.1	EST_HUMAN	QVQ-CT0225-021089-030-07 CT0225 Homo sapiens cDNA
3500	16687	29877	1.8	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCJ_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16939	28972	0.94	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6765	19921	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	z033b08.r1 Striatagene colon (#637204) Homo sapiens cDNA clone IMAGE:588663 5'
7534	20507	34082	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8143	21225	34745	5.58	5.0E-04	AI168382.1	EST_HUMAN	q13f06.x1 Soares_placenta_8f08weeks_2N8P8f08W Homo sapiens cDNA clone IMAGE:1723615 3' similar to gb-X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8498	21579	35115	0.95	5.0E-04	AA814519.1	EST_HUMAN	db9602.s1 NCJ_CGAP_G081 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element
9477	22534	36098	1.67	5.0E-04	AA848545.1	EST_HUMAN	q15903.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9571	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9718	22763	36354	0.54	6.0E-04	P28128	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYL A PRECURSOR
9809	22849	36428	4.78	5.0E-04	AW270938.1	EST_HUMAN	xe06402.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10484	23519		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11220	24289		1.9	6.0E-04	AL048607.2	EST_HUMAN	DKFZp586M2024_r1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp586M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:913875
12872	25981		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
690	13874	26907	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
870	14046	27112	1.55	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1493	14648	27728	5.58	4.0E-04	AW753358.1	EST_HUMAN	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: ltae3) Homo sapiens cDNA clone DKFZp434D059 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	Q98015	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	15407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16537	29583	0.60	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Bsrhead cdon HPLUB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
3443	16611	29629	0.6	4.0E-04	AV69624.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE. ;
4443	17583	30561	3.24	4.0E-04	AA576331.1	EST_HUMAN	AV69624 GK Homo sapiens cDNA clone GKCFH07 5'
4443	17583	30562	3.24	4.0E-04	AA576331.1	EST_HUMAN	nt10a10.a1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:961930 3' similar to gb:M21121 T-CELL
4859	17795	30781	2.33	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5193	18320	31289	3.62	4.0E-04	BE560660.1	EST_HUMAN	zn61c08.a1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562870 3'
7418	20496	33965	1.55	4.0E-04	P48442	SWISSPROT	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7705	20770	34456	0.85	4.0E-04	AL161566.2	NT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7898	20948	34456	0.8	4.0E-04	AU122079	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	AU122079 MAMMAT Homo sapiens cDNA clone MAMMA1001620 5'
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	601875885F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
8892	22932	36515	3.37	4.0E-04	A1026999.1	EST_HUMAN	w38a12.l1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264142 5'
10045	23083		1.12	4.0E-04	AF022855.1	NT	ov87b03.a1 Soares_belle_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
12691	25908		1.56	4.0E-04	AF254822.1	NT	Mus musculus neuropilin-2(at7) mRNA, alternatively spliced, complete cds
160	13385	28415	3.21	3.0E-04	AL119426.1	EST_HUMAN	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
200	13423	28454	1.7	3.0E-04	P49259	SWISSPROT	DKFZp781J221.J1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp781J221 5'
603	14078	27144	1.63	3.0E-04	U83991.1	NT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1886	15030	28137	1.7	3.0E-04	A1262100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1801	15044		0.97	3.0E-04	A1399874.1	EST_HUMAN	q228a03.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
3383	16554	29568	4.35	3.0E-04	P25147	SWISSPROT	h23a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
4071	17227	30234	4.94	3.0E-04	P48448	SWISSPROT	INTERNALIN B PRECURSOR
4187	17317		1.36	3.0E-04	AJ271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4205	17354		1.06	3.0E-04	BE140009.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4635	17771		1.18	3.0E-04	BE148846.1	EST_HUMAN	RCO-HT0014-310598-028 HT0014 Homo sapiens cDNA
4937	18087		5.2	3.0E-04	BE163778.1	EST_HUMAN	MIR0-HT0241-030200-008-c01 HT0241 Homo sapiens cDNA
5004	18133	31107	0.65	3.0E-04	AW837723.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
8271	19445		5.58	3.0E-04	AL163281.2	NT	QV3-DT0045-221295-048-D0045 Homo sapiens cDNA
6959	20187	33811	1.54	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C081

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.67	3.0E-04	AW853981.1	EST_HUMAN	RC4-NN0027-060400-011-508 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35065	2.16	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23162	36760	1.26	3.0E-04	AA454055.1	EST_HUMAN	z48408.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10381	23416	37025	0.46	3.0E-04	AI892139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.99	3.0E-04	AA781201.1	EST_HUMAN	a124905.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'; RIBOSOMAL PROTEIN L7A (HUMAN); nc38a04.r1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1 L2 L1 repetitive element;
12249	26164	31655	2.39	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12646	25887	31769	2.54	3.0E-04	AB018292.1	NT	DKFZp547L186_r1 547 (synonym: hfor1) Homo sapiens cDNA clone DKFZp547L186 5'
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
180	13403	26432	1.33	2.0E-04	AF217798.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
491	13685	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	Human dystrophin gene
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
930	14105	27168	5.02	2.0E-04	M86524.1	NT	qH88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1206	14368		2.78	2.0E-04	AI286021.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1213	14374		2.6	2.0E-04	AL163203.2	NT	Mus musculus 5' flanking region of Plb3 gene
1879	15023		1.71	2.0E-04	AF224268.1	NT	z139505.c1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2257	15390		1.21	2.0E-04	AA478980.1	EST_HUMAN	
2641	15764	28578					Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV15S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV35S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
3052	16228	29248	6.42	2.0E-04	U66061.1	NT	
3415	16584	29600	1.23	2.0E-04	AI124528.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539780 3'
3622	16898	29697	0.82	2.0E-04	BE082317.1	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
4022	17178	30187	2.58	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070600-194-b07 BT0638 Homo sapiens cDNA
4281	17406		0.98	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4791	17928	30914	5.5	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4791	17928	30914	1.76	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17928	30915	1.76	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4816	18048		1.22	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18283	31256	1.47	2.0E-04	AB037697.1	NT	Danio rerio heparinase gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF067016.1	NT	Dicotyledon discoidium interaphin (abpD) gene, complete cds
5661	18855	32138	1.11	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCJH10.3
5674	18868	32154	1.83	2.0E-04	AB090862.1	EST_HUMAN	lc03b1.1.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709.3
5668	19059	32386	0.93	2.0E-04	AA296662.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6008	19250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6068	19538	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000768.5
7478	20583		0.84	2.0E-04	AW860963.1	EST_HUMAN	QV0-CT0387-180300-187-e10 CT0387 Homo sapiens cDNA
7798	20854		13.66	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20863	34357	1.45	2.0E-04	P64296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD T11N-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35084	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8841	22020	35561	0.67	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
8535	22600	36173	0.88	2.0E-04	AA726700.1	EST_HUMAN	al22a12.61 Soares testis NHT Homo sapiens cDNA clone 1343518.3
8919	22674	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1
10180	23217	36808	1.16	2.0E-04	BE149303.1	EST_HUMAN	RC3-H10254-161059-011-b05 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	zu66ct1.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:742964.5
11088	24162	37798	3.88	2.0E-04	AV793073.1	EST_HUMAN	AV793073 HTF Homo sapiens cDNA clone HTFAA01.5
11895	24638	38318	2.68	2.0E-04	AA440282.1	EST_HUMAN	l01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269.3 similar to contains Alu repetitive element
11710	24760	38443	2.36	2.0E-04	AW136740.1	EST_HUMAN	UHH-B11-adm-c-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:271790.3
11859	24847		2.71	2.0E-04	BE085781.1	EST_HUMAN	RC2-BT0317-150200-011-404 BT0317 Homo sapiens cDNA
12706	25086	38790	32.04	2.0E-04	P21733	SWISSPROT	HYPOTHETICAL 29.1 KD PROTEIN IN CRYB1 5 REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13181	28179		1.28	2.0E-04	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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788	13967	27018	0.86	1.0E-04	H99646.1	EST_HUMAN	yc26c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.H1 L1 repetitive element;
1100	14265	27322	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
1138	14303	27358	3.79	1.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1 st NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1 st NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62918.1	NT	Arginella anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1857	14910	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1857	14910	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TTY36
2752	15869	28978	1.08	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176386 3'
2752	15869	28979	1.08	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176386 3'
3356	16528	29543	1.18	1.0E-04	Q92203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3829	16989	29992	0.85	1.0E-04	AI440282.1	EST_HUMAN	IQ1111.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140288 3' similar to contains Alu repetitive element;
4171	17521	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17542	30335	1.12	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLC8BD04 3'
5207	18328	31288	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19165	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.st NCL CGAP_P13 Homo sapiens cDNA clone IMAGE:252
6977	20205	33633	0.86	1.0E-04	AA594581.1	EST_HUMAN	h125a04.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb.M87252
7336	20417	33879	12.52	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7744	20417	33879	13.48	1.0E-04	AI251980.1	EST_HUMAN	q657d10.x1 NCL CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21268	34789	1.02	1.0E-04	A4630453.1	EST_HUMAN	q657d10.x1 NCL CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
9598	22803	36175	2.75	1.0E-04	AI808220.1	EST_HUMAN	ab94g08.s1 Simulagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9548	22813	36182	1.54	1.0E-04	Q88989	SWISSPROT	w28e08.x1 Soares NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:2356742 3'
9525	22880		0.76	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9846	22886	36466	1.05	1.0E-04	10863876	NT	yt72c08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:113774 5'
							Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23495	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11822	24673		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24636	38837	1.81	1.0E-04	AB032988.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24676	36680	1.94	1.0E-04	AW269061.1	EST_HUMAN	xx49g12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
719	13898	26938	2.44	9.0E-05	AA718933.1	EST_HUMAN	af45c11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1292468 3'
4198	17346	30338	1.13	9.0E-05	A1762209.1	EST_HUMAN	wf4c11.x1 NCI_CGAP_Cor18 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER8.1
6084	19268	32596	1.37	9.0E-05	Q60716	SWISSPROT	MER8 repetitive element; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34301	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1-H-B1-aar-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720288 3'
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1-H-B1-aar-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9677	22639		3.03	9.0E-05	D65608.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
9679	22841	36211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_B118 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
11518	24574	38251	1.61	9.0E-05	A1287878.1	EST_HUMAN	q23106.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
11918	19266	32595	3.41	9.0E-05	Q60716	SWISSPROT	MIR repetitive element; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12469	26016		3.37	9.0E-05	AF128758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDHA, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, IC7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251846.1	NT	Plum salivum mRNA for beta-1,3 glucanase (gns2 gene)
887	14063		3.11	8.0E-05	AJ251846.1	NT	Plum salivum mRNA for beta-1,3 glucanase (gns2 gene)
3015	16181		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4804	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Scores_NSIF_F8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:2554638 3'
8948	22027	35568	0.51	8.0E-05	Y11666.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11419	24480	38146	2.58	8.0E-05	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13159	26001		1.78	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu
357	13568	26598	3.16	7.0E-05	AW847445.1	EST_HUMAN	repetitive element; contains element MSR1 repetitive element;
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-C10208-220698-011-E04 C10208 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
561	13773	26793	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
561	13773	26794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1060	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15669	28008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dicysteleium discoidium gene for TRFA, complete cds
4168	17318		0.85	7.0E-05	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30614	1.88	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5041	18169	31144	0.88	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505582.1	EST_HUMAN	rhes3g01.s1 NCL CGAP_Br2 Homo sapiens cDNA clone IMAGE:966098 3'
9753	22691	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Striatum (cat8836206) Homo sapiens cDNA clone HFBED60
11430	24491		5.87	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2063	16223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	16223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28892	1.56	6.0E-05	AI655241.1	EST_HUMAN	WB54h08.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03260 DNA TOPOISOMERASE I (HUMAN);
2878	13880	28912	2.54	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32538	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6333	18997	33070	1.6	6.0E-05	N72829.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA897680.1	EST_HUMAN	q80a03.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8276	21358	34876	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
8638	21718	35255	0.82	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491728 3' similar to contains element MER28 repetitive element;
8643	21723	35260	2.62	6.0E-05	AW896629.1	EST_HUMAN	PMA-NN0050-310300-001-F10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DEGRADATION-ACCELERATING FACTOR PRECURSOR
9452	22568	36134	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9482	22668	36135	1.59	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22785	36357	1.77	6.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Striatum lung (#637210) Homo sapiens cDNA clone IMAGE:119062 5'
9922	22862	36550	0.69	6.0E-05	AW627985.1	EST_HUMAN	h137a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10987	24066	37701	2.42	6.0E-05	R75639.1	EST_HUMAN	y169d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains L1 TR1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38495	2.7	6.0E-05	AA044015.1	EST_HUMAN	zK8602.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12699	25599	31773	9.37	6.0E-05	AW690110.1	EST_HUMAN	MRO-NT0038-250400-001-069 NT0038 Homo sapiens cDNA
1435	14588	27661	20.97	5.0E-05	AW392088.1	EST_HUMAN	QV4-ST0234-241189-040-111 ST0234 Homo sapiens cDNA
1912	18055		1.07	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2824	18102	29118	0.84	5.0E-05	AJ251058.1	NT	Homo sapiens MEF1A gene, promoter region and exon 1
4088	17243	30250	3.16	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6116	19295	32630	3.58	5.0E-05	AV693544.1	EST_HUMAN	AV693544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6287	19470	32825	0.97	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7485	20560		1.4	5.0E-05	AB037984.1	NT	Mus musculus gene for calretinin, exon 1
12468	25503		5.28	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868	13457		2.73	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4605	17742	30720	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4805	17742	30721	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4997	18126		0.95	4.0E-05	AF164488.1	NT	Cyclosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18256	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
9723	22788		6.75	4.0E-05	AF202635.1	NT	Homo sapiens PP-1200 mRNA, complete cds
10817	23651	37280	0.54	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (AGID BETA-GALACTOSIDASE)
11007	24086	37723	4.14	4.0E-05	AW627948.1	EST_HUMAN	h18607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element:
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C062
12428	25302		1.47	4.0E-05	AW117580.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
13189	25773		1.16	4.0E-05	AA417556.1	EST_HUMAN	z01e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
698	13881	26914	0.8	3.0E-05	AI248061.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element: contains element KER repetitive element:
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16537		0.7	3.0E-05	AI288919.1	EST_HUMAN	q01g11.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4501	17641	30625	7.91	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4501	17641	30626	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4558	17725	30707	1.11	3.0E-05	AA388678.1	EST_HUMAN	EST79998 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4588	17725	30708	1.11	3.0E-05	AA368679.1	EST_HUMAN	EST19896 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4959	13881	26014	0.7	3.0E-05	AI248091.1	EST_HUMAN	qf64c10.x1 Soares fetal liver screen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849433 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
5675	18569	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myf2p), mRNA
6897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE733167.1	EST_HUMAN	601587.451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8547	21628	35166	1.55	3.0E-05	AA284049.1	EST_HUMAN	zs60005.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9094	22173	35718	1.56	3.0E-05	AW770982.1	EST_HUMAN	H94e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9098	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22586	36154	1.4	3.0E-05	AA372562.1	EST_HUMAN	EST184475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22803		3.62	3.0E-05	AJ766331.1	EST_HUMAN	wg36f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10755	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric and
12561	25374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12913	26196		1.29	3.0E-05	AW518689.1	EST_HUMAN	xs89d06.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2400	15531	28658	1.49	2.0E-05	AI286021.1	EST_HUMAN	qf88e11.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2776811 3'
2650	15773	28886	14.63	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element ;
						NT	Human edonine deaminase (ADA) gene, complete cds
2777	15893		6.99	2.0E-05	AA160562.1	EST_HUMAN	zq48a12.r1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3207	16382	29393	1.29	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-008 BT0319 Homo sapiens cDNA
3429	16597	29613	1.04	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3583	16748		0.87	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3908	17068		0.81	2.0E-05	AL039107.1	EST_HUMAN	DKFZ5681064.r1 568 (synonym: hnf2d2) Homo sapiens cDNA clone DKFZ5681064 5'
5003	18132	31106	0.6	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5878	18068	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6039	19222		0.87	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6288	19459	32811	0.79	2.0E-05	A149272.1	EST_HUMAN	gc72a02.x1 Soares_placenta_8tc0weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'
6760	19916	33311	2.11	2.0E-05	AA714930.1	EST_HUMAN	similar to contains L1.63 L1 repetitive element:
7042	20096	33511	1.69	2.0E-05	Y08926.1	NT	hw08d12.at NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7054	20107	33523	1	2.0E-05	A1492960.1	EST_HUMAN	P.falcipterus mRNA for AARF1 protein, partial
7062	20115		7.24	2.0E-05	A1991026.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:20300003 3' similar to TR:Q02711
7303	20385	33844	2	2.0E-05	AF224262.1	NT	002711 PRO-POL-DUTPASE POLYPROTEIN:
7303	20385	33845	2	2.0E-05	AF224262.1	NT	wu35i07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7524	20587	34671	0.77	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
8069	21161	34671	1.93	2.0E-05	A1981040.1	EST_HUMAN	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
9467	22524	36087	0.68	2.0E-05	P49457	SWISSPROT	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9467	22524	36088	0.56	2.0E-05	P49457	SWISSPROT	ig20f05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
10127	23185	36764	0.6	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10339	23374	36984	0.94	2.0E-05	BF055939.1	EST_HUMAN	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C007
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10891	20115		2.66	2.0E-05	A1991025.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8tc0weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
11738	23924	37549	1.55	2.0E-05	BE175801.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8tc0weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
11981	24986	38688	5.74	2.0E-05	A1912713.1	EST_HUMAN	wu35f07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
12477	25921		3.7	2.0E-05	BE348229.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12592	28104		8.13	2.0E-05	AW074604.1	EST_HUMAN	wel2hd05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921 3'
							hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2:
							xa89a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.63 L1 repetitive element:

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12650	25905		3.24	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25531	32014	2.01	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13206	25787		1.64	2.0E-05	AI200970.1	EST_HUMAN	qf69g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2759	16071	28983	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	25905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Larmito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3815	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens caldium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17535	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	z069g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4875	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5078	18207	31179	0.86	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.84	1.0E-05	Z18943.1	NT	H.sapiens repeat region
6881	20043	33451	1.13	1.0E-05	AJ248003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20135	33553	4.24	1.0E-05	AA841846.1	EST_HUMAN	hs19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1
7232	20318	33759	5.19	1.0E-05	4605944	NT	L1 repetitive element;
7837	20892	34394	0.73	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
9116	22195		2.39	1.0E-05	AL163227.2	NT	MER10 repetitive element;
9280	22337	36887	2.59	1.0E-05	AA452578.1	EST_HUMAN	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9487	22544	36107	12.29	1.0E-05	AA236110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9596	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	z035h12.s1 Soares_testis_fetus_NB2Hf8_9w Homo sapiens cDNA clone IMAGE:786519 3' similar to
10043	23081	36682	0.79	1.0E-05	AW510902.1	EST_HUMAN	gb102832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10043	23081	36683	0.79	1.0E-05	AW510902.1	EST_HUMAN	z050e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:884332 5' similar to contains Alu
10120	23158	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	repetitive element; contains element TAR1 repetitive element;
10120	23158	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	AV732180 HTF Homo sapiens cDNA clone HTFBIH01 5'
10387	23422		2.04	1.0E-05	AW466985.1	EST_HUMAN	hcd1b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.11 OFR repetitive element;
							hcd1b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
							OFR.11 OFR repetitive element;
							UIH-B12-egk-a-08-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							UIH-B12-egk-a-08-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
							hcd7c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1
							repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11159	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	26036	31663	1.4	1.0E-05	AL163303.2	NT	Human sapiens chromosome 21 segment HS21C103
2737	18854	28968	5.83	9.0E-06	AI583811.1	EST_HUMAN	H73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3165	16340	29348	6.11	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1759191 3'
3698	16859		2.58	9.0E-06	M51755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6025	19208	32528	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7596	20668	34144	2.82	9.0E-06	P08347	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7953	21003	34515	12.35	9.0E-06	AI034370.1	EST_HUMAN	cc20g01.x1 Soares_fetal_liver_spleen_TNPLS_ST Homo sapiens cDNA clone IMAGE:1656812 3' similar to contains Alu repetitive element
8659	21739	35280	1.17	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
9183	22281	35803	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22251	35804	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37853	3.51	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2596	16065	28839	2.01	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201198-011-H1 CT0283 Homo sapiens cDNA
6728	19894	33276	2.75	8.0E-06	AA284847.1	EST_HUMAN	z22d05.s1 Soares ovary tumor NihOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MERA11 MER20 repetitive element
10751	23784	37957	0.69	8.0E-06	P34083	SWISSPROT	FASIGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASIGLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA689729.1	EST_HUMAN	al60f10.s1 Stratigene lung (#637210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element
1470	14624	27708	3.12	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2836	16113		10.58	7.0E-06	AI568252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element
3564	16817		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST189205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	18003		6.49	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250-00-173-h01 OT0062 Homo sapiens cDNA
5925	19112	32424	0.93	7.0E-06	N08845.1	EST_HUMAN	y65c07.r1 Soares_multiple_sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:278412.5
8989	22068	35608	0.83	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF88S1E), mRNA
10104	23142		0.52	7.0E-06	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	28131	31547	1.63	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972.5
2984	16160	29177	1.17	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3784	16946	29652	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4876	16183	29206	2.13	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4883	18013	30997	2.19	6.0E-06	A1040099.1	EST_HUMAN	cd08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738.3 similar to contains MER.12 MER.8 repetitive element;
5405	18665	31644	2.29	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5523	18722	31739	1.16	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10060	23098		1.99	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13142	25742	31948	2.39	6.0E-06	11416157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6186	18362	32710	3.74	6.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6487	18634	32995	1.64	6.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8654	21734	35274	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23342	36947	6.96	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
10731	23764	37372	0.61	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25668	31957	5.49	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
664	13850	28877	5.47	4.0E-06	R16287.1	EST_HUMAN	y448c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254.5 similar to contains Alu repetitive element; contains L1 repetitive element;
869	14046	27110	4.73	4.0E-06	AW103354.1	EST_HUMAN	xx69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574.3 similar to contains Alu repetitive element; contains element MER21 repetitive element;
1365	14519	27593	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168.3
1365	14519	27594	3.18	4.0E-06	A1334928.1	EST_HUMAN	ib33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168.3
1503	14656	27738	1.45	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2339	15470	28605	1.56	4.0E-06	AW015401.1	EST_HUMAN	UL14-BIG-act-f05-0-J1 s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425.3
3131	16307	29321	0.89	4.0E-06	AF198349.1	NT	Galus gallus Dach2 protein (Dach2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-06	AW848295.1	EST_HUMAN	IL3-GT0214-150200-074-B03 CT0214 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4829	18050	31041	1.89	4.0E-06	AB86939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element ;
8898	21776	35308	0.68	4.0E-06	O15933	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9000	22079	35620	4.49	4.0E-06	AF096960.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9809	22849	36335	1.28	4.0E-06	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11735	23821	37546	3.99	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
13149	26152		1.33	4.0E-06	AW289734.1	EST_HUMAN	xs53e01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15366	28494	1.31	3.0E-06	AA700582.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element ;
2232	15366	28495	1.31	3.0E-06	AA700582.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.1 L1 repetitive element ;
2340	16471		1.48	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2888	18164	29180	0.84	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element ;
3339	19512		2.87	3.0E-06	AI857779.1	EST_HUMAN	W22a05.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ; contains L1.12 L1 repetitive element ;
3883	17042	30040	1.47	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3883	17042	30041	1.47	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	y578b10.r1 Stralagene ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4684	17819	30907	5.52	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
8289	19462	32814	0.82	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
7377	20459		2.14	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8274	21356	34874	0.81	3.0E-06	BE562984.1	EST_HUMAN	601339213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3890314 5'
8883	21962	35496	0.75	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12850	25435		12.07	3.0E-06	AW385282.1	EST_HUMAN	RCOL-T0001-267199-011-A03 L70001 Homo sapiens cDNA
207	13430		2.22	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2451	15579	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	w904e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1
2537	15692	28785	1.89	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	15755	28870	1.81	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3507	16771	28786	0.9	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB03 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3858	17018	30017	1.54	2.0E-06	AA173618.1	EST_HUMAN	z02a05.r1 Stratagene ovarian cancer (#03/219) Homo sapiens cDNA clone IMAGE:595232 5'
3868	17027	30026	0.68	2.0E-06	AW450215.1	EST_HUMAN	UIH-B13-aky-g-05-0-UI.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2736176 3'
3876	17035	30033	1.7	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A10, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6246	19420	32766	0.62	2.0E-06	AF539448.1	EST_HUMAN	te51105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6571	19733	33112	5.64	2.0E-06	AB19424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7635	20704	34183	0.63	2.0E-06	AA688423.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184		1.02	2.0E-06	AW869223.1	EST_HUMAN	nv99c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1 repetitive element ;
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9049	22128	35672	1.59	2.0E-06	H62051.1	EST_HUMAN	zh27c11.s1 Soares_pineal_gland_NHPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9417	22431	36056	0.9	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9417	22461	36057	0.9	2.0E-06	AF003529.1	NT	YU37c04.r1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9436	22510		0.46	2.0E-06	AI473450.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9502	22942	36527	0.86	2.0E-06	N30570.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
10123	23161		0.7	2.0E-06	AV749989.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
12548	26135	31549	1.34	2.0E-06	P23249	SWISSPROT	W16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	yw68e03.s1 Soares_placenta_8to8weeks_2NbpHP8a9W Homo sapiens cDNA clone IMAGE:257212 3'
34	13272	26276	1.16	1.0E-06	O76092	SWISSPROT	AV749989 NPC Homo sapiens cDNA clone NPCAXD05 5'
674	13860	26891	1.8	1.0E-06	AF084394.1	NT	PROTEIN MOV-10
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:314689 3' similar to contains L1.12 L1 repetitive element ;
1553	14706	27788	1	1.0E-06	AL168278.2	NT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	Mus musculus D6M5E protein (D6M5e) mRNA, complete cds
1603	14756	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN CMZ-8
							Homo sapiens chromosome 21 segment HS21C078
							z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
							z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1815	14763		0.69	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NGF1) gene, complete cds
2050	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NGF1) gene, complete cds
4489	17629	30610	15.97	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b and putative M8604 Met protein (M8604 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18465	31422	0.72	1.0E-06	N65948.1	EST_HUMAN	z427408.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:283750 3'
5405	18607	31579	5.14	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6915	19103		0.72	1.0E-06	BE063527.1	EST_HUMAN	GM0-BT0281-031159-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A) CHAIN PRECURSOR
7923	28223		0.73	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8100	21272		0.99	1.0E-06	AA912623.1	EST_HUMAN	o28c-08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1624878 3'
8468	21549	35079	1.12	1.0E-06	AI347010.1	EST_HUMAN	qp54e02.x1 NCI CGAP_Oc8 Homo sapiens cDNA clone IMAGE:1926842 3'
8985	21765	35297	1.31	1.0E-06	AI287878.1	EST_HUMAN	qy2308.x1 NCI CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
8985	21765	35297	1.31	1.0E-06	AI287878.1	EST_HUMAN	NIR repetitive element ;
9504	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	z565601.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:286472 3'
9579	22721	36291	0.81	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22969	36558	5.22	1.0E-06	AA132611.1	EST_HUMAN	z017e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	z044d11.s1 Soares_fetal_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:785493 3' similar to
10705	23738		2.19	1.0E-06	AL163203.2	NT	gbD26128 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11849	24935		3.1	1.0E-06	AW890941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12589	25396	32041	8.24	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8502	21683		0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
4893	18023	31008	4.23	8.0E-07	AI288698.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
							q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4893	18023	31009	4.23	8.0E-07	A1285596.1	EST_HUMAN	q182p07.x1 Scores, NHMPu.S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6007	19192		8.17	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8191	21273		8.44	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11021	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat836206) Homo sapiens cDNA clone HFBEN69
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31906	0.86	7.0E-07	6003700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6006700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1962	15105	28205	3.47	6.0E-07	AW855558.1	EST_HUMAN	CV3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2561	15686	28812	2.43	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	799407.x1 NCL_CGAP_C016 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:075920 075920 4F6L.
12115	25095	38800	1.45	6.0E-07	BE063609.1	EST_HUMAN	CM0-BT0281-031198-087-a03 BT0281 Homo sapiens cDNA
12444	26087		1.72	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-H12 NN1029 Homo sapiens cDNA
13229	25992		1.32	6.0E-07	BE222390.1	EST_HUMAN	hu11h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166329 3' similar to contains L1, b2 L1 L1 repetitive element
336	13549		1.04	5.0E-07	A831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14248		2.39	6.0E-07	AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
3096	16272		0.73	5.0E-07	A831893.1	EST_HUMAN	wh64f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4769	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	19421	32767	1.33	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7210	20075	33487	1.71	5.0E-07	A393981.1	EST_HUMAN	Ig06505.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element
7210	20075	33488	1.71	5.0E-07	A393981.1	EST_HUMAN	Ig06505.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element; contains element A3R repetitive element
7503	20578	34050	16.93	5.0E-07	AW070886.1	EST_HUMAN	xa31e02.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:U15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8687	21797		0.88	5.0E-07	P09563	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23612	37217	5.47	5.0E-07	AI089597.1	EST_HUMAN	CM-BY178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24688		2.08	5.0E-07	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12256	25988		1.2	5.0E-07	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21: C085
12918	25966		3.06	5.0E-07	AW1862537.1	EST_HUMAN	QV0-GT0383-210400-204-b12 GT0383 Homo sapiens cDNA
4108	17260	30261	1.68	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCL_CGAP_C083 Homo sapiens cDNA clone IMAGE:2604697.3
7328	20410		0.8	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20485	33963	0.97	4.0E-07	Q822V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20485	33964	0.97	4.0E-07	Q922V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9251	22328	35875	4.9	4.0E-07	AW419134.1	EST_HUMAN	xy48g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548.3
10332	23367	36976	0.53	4.0E-07	BE601975.1	EST_HUMAN	601876748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959681.5
10332	23367	36977	0.53	4.0E-07	BE601975.1	EST_HUMAN	601876748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959681.5
10531	23555	37174	0.55	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	AJ765528.1	EST_HUMAN	w81b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11179	24248	37882	3.88	4.0E-07	AJ765528.1	EST_HUMAN	w81b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11495	24553		1.69	4.0E-07	BE001928.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
11919	24905		1.32	4.0E-07	BE967557.1	EST_HUMAN	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932924.5
13207	25788		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26886	5.39	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
506	13788	26806	3.59	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1405	14559	27833	1.43	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1655	14808		3.62	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 019 allele
2104	15243		2.32	3.0E-07	AA528763.1	EST_HUMAN	n156b09.e1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element contains L1.13 L1 repetitive element
2361	15482	28621	1.14	3.0E-07	M98149.1	NT	Human polymorphic microsatellite DNA
2540	15855	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2540	15855	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3098	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	xy50f12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111605.6
3228	16402	29414	1.78	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT-LRMT INTERGENIC REGION PRECURSOR
4802	17937		0.64	3.0E-07	P20740	SWISSPROT	OVSSTATIN PRECURSOR (OVOMACROGLOBULIN)
4849	17982	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLG Homo sapiens cDNA clone GLCC001.3
4885	18015	30959	0.7	3.0E-07	AJ797286.1	EST_HUMAN	w86b12.x1 Soares_NFL_T_GBC, St Homo sapiens cDNA clone IMAGE:2347967.3

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5175	18297	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18297	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5783	18975	32281	12.39	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6095	19276	32605	0.7	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	19995		5.09	3.0E-07	A4815175.1	EST_HUMAN	cc04c10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7678	20743	34224	3.53	3.0E-07	AW797168.1	EST_HUMAN	QV1-LM0038-200300-115-g02 UM0036 Homo sapiens cDNA
7841	20896		1.3	3.0E-07	A1591065.1	EST_HUMAN	tw28f11.x1 NCL CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9330	22406	35959	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9330	22406	35960	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13104	25777		4.26	3.0E-07	AJ132382.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
29	13267	26270	7.32	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26413	6.06	2.0E-07	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
158	13383	26414	6.06	2.0E-07	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic/vascular actin gene, complete cds
767	13948	26995	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
767	13948	26996	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
966	14139	27200	2.32	2.0E-07	AA223280.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
967	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element ;
1189	14361	27409	1.55	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1630	14782	27898	2.06	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3708	18869		0.63	2.0E-07	BF131397.1	EST_HUMAN	601818016F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3779	18940	29946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-h11 NN1023 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6460	18630	31638	1.52	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	26828	33229	0.73	2.0E-07	AW448968.1	EST_HUMAN	U1-H-B13-aka-b-01-O-U1.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734008 3'
8602	19857	33357	3.39	2.0E-07	AI208715.1	EST_HUMAN	q95605.x1 Soares_Testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8684	21744		3.87	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAE302 5'
8693	21972	35508	1.11	2.0E-07	AA035198.1	EST_HUMAN	2227909.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
8963	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23508	37122	6.34	2.0E-07	AW892507.1	EST_HUMAN	OM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10706	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12138	26855		2.96	2.0E-07	BE153717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12226	25987		2.38	2.0E-07	AI732482.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
1126	14291		0.76	1.0E-07	AL163282.2	NT	PM0-FT0339-260100-006-f07 HT0339 Homo sapiens cDNA
2888	14704	27784	2.08	1.0E-07	P09256	SWISSPROT	z055111.x5 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:555029 3' similar to contains THR.b2 THR repetitive element
3838	14291		1.24	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4408	17650	30534	2.91	1.0E-07	AV718662.1	EST_HUMAN	GLYCOPROTEIN GPV
4408	17650	30535	2.91	1.0E-07	AV718662.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
6632	19751	33180	0.8	1.0E-07	U82671.2	NT	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
7006	20142	33580	4.69	1.0E-07	BE047871.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7006	20142	33581	4.69	1.0E-07	BE047871.1	EST_HUMAN	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7682	20729	34205	7.6	1.0E-07	N55081.1	EST_HUMAN	tz43d08.y1 NCL_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281339 5'
7826	20881	34382	0.69	1.0E-07	BF375809.1	EST_HUMAN	yv43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7826	20881	34383	0.69	1.0E-07	BF375809.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7854	20808	34413	1.24	1.0E-07	AL163281.2	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	Homo sapiens chromosome 21 segment HS21C081
8410	21491	35021	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9155	22233	35778	2.7	1.0E-07	AA063576.1	EST_HUMAN	z051e10.s1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:434346 3'
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TSS) (METH-2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36436	0.6	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36776	2.35	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element ;
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	80213714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10682	23716		1.22	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12085	25066	38771	2.35	1.0E-07	AI341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12506	25639	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2006892 3'
12856	25438		1.45	1.0E-07	X64487.1	NT	hr53c11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 O65722
12852	25566		2.1	1.0E-07	X51755.1	NT	DJ1168J1.1 ;
7433	20510	33982	0.75	9.0E-08	AI63362.1	EST_HUMAN	H.sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	le61b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090185 3'
11965	24950	38656	2.38	9.0E-08	AI163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABFB06 5'
12456	25320		2.51	9.0E-08	AJ251973.1	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446532 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911362.1	EST_HUMAN	OFR repetitive element ;
1075	14241		1.01	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3634	16798		1.57	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steirin-1 gene
8837	22016	35557	5.35	8.0E-08	AI752367.1	EST_HUMAN	wd16505.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22016	35558	5.35	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8927	22867	36449	3.03	8.0E-08	AW970693.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11523	24579		1.73	8.0E-08	AF253417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
82	13317	26345	3.91	7.0E-08	Q02357	SWISSPROT	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Homo sapiens lun dimerization protein gene, partial cds; cbs gene, complete cds; and unknown gene
3666	18826	29839	0.88	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3666	18826	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
5332	18445	31413	0.62	7.0E-08	T65891.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11970	24955	38658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)

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12978	16829	28839	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16829	28840	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15564	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT0165-191199-004-g09 HT0166 Homo sapiens cDNA
3129	16305	28919	0.68	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4383	17806	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9529	22564		0.55	6.0E-08	AA827076.1	EST_HUMAN	cb56605.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24688	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11823	24812		1.43	6.0E-08	AL163209.2	NT	ENDONUCLEASE
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2309	16441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	nt03609.s1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	26271	32077	1.77	6.0E-08	AW861878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1799	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2950	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5' contains Alu repetitive element;
3132	16308		1.01	4.0E-08	AI078417.1	EST_HUMAN	cd56e02.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674456 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U82666.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6535	19698	33071	1.07	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8998	22077	35617	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEIN, SERINE 2
9340	22416	35969	1.13	4.0E-08	L42571.1	NT	Orf100 ribosomal transcription factor (UBF2) mRNA, complete cds
9845	22885		1.56	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10536	23571		0.85	4.0E-08	AI016342.1	EST_HUMAN	cl78d12.s1 Soares fetal_liver_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622903 3'
10597	23632	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	en22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1669411 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA398327.1	EST_HUMAN	z7f6b08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA,K-EXCHANGER ;

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11328	24391	38038	5.16	4.0E-08	AA393627.1	EST_HUMAN	z776b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11349	24411	38004	11.86	4.0E-08	BF692493.1	EST_HUMAN	G505579 NA/CA_KEXCHANGER ;
11349	24411	38005	11.86	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	26108		1.93	4.0E-08	W76159.1	EST_HUMAN	z186g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L.1.1 L1 repetitive element ;
12804	25598		2.01	4.0E-08	A1343553.1	EST_HUMAN	1895a11.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
5728	18921	32215	2.27	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17 ;
7115	18541	31488	6.01	3.0E-08	A1792737.1	EST_HUMAN	q57611.y5 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:1944045 5'
7711	20776	34262	1.43	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS2TC046
7828	20978		3.32	3.0E-08	A1436352.1	EST_HUMAN	th93h09.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
10102	23140		0.63	3.0E-08	AF050666.1	NT	Homo sapiens MHC class 1 region
11276	24343	37983	1.64	3.0E-08	A1218001.1	EST_HUMAN	q121a04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1845294 3'
11957	24942	38646	1.32	3.0E-08	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
12156	25125		33.85	3.0E-08	R18420.1	EST_HUMAN	y912104.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element ;
211	13434		4.16	2.0E-08	AW302896.1	EST_HUMAN	z87705.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3'
236	13458		5.76	2.0E-08	AA425598.1	EST_HUMAN	zw48707.r1 Soares_fetal_fetus_Nb2HF8_9W Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element ; contains element MER16 repetitive element ;
509	13703	26732	4.46	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 mRNA, complete cds
677	13863	26883	9.7	2.0E-08	AW886438.1	EST_HUMAN	MF0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
677	13863	26894	9.7	2.0E-08	AW886438.1	EST_HUMAN	MF0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	14186		7.75	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3135893 5'
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS2TC047
1774	14923	28017	0.98	2.0E-08	AW841860.1	EST_HUMAN	IL5-CN0024-030300-028-C01 CN0024 Homo sapiens cDNA
1760	14929		2.08	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC 27 Homo sapiens cDNA clone IMAGE:3845199 5'
1902	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	z433f11.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2608	15732		1.86	2.0E-08	K00216.1	NT	Sheep His-4RNA-GUG
3279	16453	29474	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR

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3278	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3662	17120		1.63	2.0E-08	AV1813620.1	EST_HUMAN	RC3-ST0197-161099-012-403 ST0197 Homo sapiens cDNA
4189	17339	30332	0.62	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17664		1.48	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:874380 5' similar to contains L1.12 L1 repetitive element ;
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	ab0h11.e1 Soares_besla_NHT Homo sapiens cDNA clone 1377189 3'
5955	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xd82c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2598462 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
8193	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8301	21383	34804	1.5	2.0E-08	AA480121.1	EST_HUMAN	ab02g06.e1 Stratiens fetal retina B37202 Homo sapiens cDNA clone IMAGE:839674 3'
9286	22362		0.89	2.0E-08	AU139978.1	EST_HUMAN	AU139978 PLAGE1 Homo sapiens cDNA clone PLAGE1011719 5'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10798	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
12478	25328		1.77	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
13085	28159		1.8	2.0E-08	11431878	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1538	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE] (TRANSCRIPTION FACTOR NTF-1)
1672	14824	27907	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1672	14824	27908	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
1816	14855	28058	1.66	1.0E-08	AF125348.1	NT	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
2110	15248		2.97	1.0E-08	BE141959.1	EST_HUMAN	PM2-H10130-150999-001-112 HT0130 Homo sapiens cDNA
3261	16435	29453	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D6232 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3261	16435	29454	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D6232 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5718	18909	32204	4.51	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7948	20986	34507	0.94	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8224	21306	34828	0.62	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102

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8320	21402	34927	0.54	1.0E-08	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	AI015304.1	EST_HUMAN	(UBE2D3) genes, complete cds
9405	22479		0.56	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10778	23811	37434	0.87	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11595	24848	38332	3.55	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12581	25391		3.06	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
13137	25925		1.26	1.0E-08	BF375396.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	MR4-S10240-240700-013-g04 S10240 Homo sapiens cDNA
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10287	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7414	20492	33960	8.1	8.0E-09	AI183500.1	EST_HUMAN	ye58a12 s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:121918 3'
8189	21271	34786	2.54	8.0E-09	AW900159.1	EST_HUMAN	contains MSR1.1t MSR1 repetitive element
9189	22267		2.53	8.0E-09	AA938892.1	EST_HUMAN	op74d08 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1592575 3'
3695	16856		1.98	7.0E-09	D96842.1	NT	Homo sapiens DNA for 3-Meoxacy-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4115	17269		0.98	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8086	21168		0.58	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element
9460	22517	36080	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254650.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10554	23589		0.76	7.0E-09	AA058626.1	EST_HUMAN	zr58e07 s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element
10910	23993		2.01	7.0E-09	T97950.1	EST_HUMAN	ye58a12 s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:121918 3'
2221	15355		0.96	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5496	18695	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	xr85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35396	1.11	6.0E-09	BE161663.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10989	24049	37682	1.66	6.0E-09	BF108765.1	EST_HUMAN	745610.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12089	25089	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003762 Human adult (K.Okubo) Homo sapiens cDNA
1447	14900	27677	3.47	6.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1900	15043	28154	7.4	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6540	19703	33075	2.22	5.0E-09	AA359454.1	EST_HUMAN	EST168746 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6988	18507	31523	0.66	5.0E-09	U66059.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8785	21864	35407	0.63	5.0E-09	P37071	SWISSPROT	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
10300	23335	36940	3.25	5.0E-09	AW799667.1	EST_HUMAN	z60609.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795880 3'
11944	24930	38632	1.87	5.0E-09	AA460142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens hypothetical protein (AF038199), mRNA
1487	14850	27732	1.86	4.0E-09	9558718	NT	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2500	15027	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	z604c06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	yd11a07.s1 Soares_fetal liver spleen TNFALS Homo sapiens cDNA clone IMAGE:66804 3'
8718	21769	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	wt94f10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11330	24383	38041	9.51	4.0E-09	AI886401.1	EST_HUMAN	zr34e12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807
11379	24440		1.44	4.0E-09	AA195142.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
2427	15555	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2819	15742	28858	1.06	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2716	15834	28944	0.69	3.0E-09	P23249	SWISSPROT	hu09a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	PROTEIN MOV-10
							hu09a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							MER18 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3464	16631		0.7	3.0E-09	AA442272.1	EST_HUMAN	z646d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17381		0.62	3.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4546	17694	30668	3.47	3.0E-09	AF17525.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4634	17770	30761	1.19	3.0E-09	Q8Y3R5	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0893)
8084	21166	34882	1.1	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194080 3' similar to TR-O65091
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	O65091 IMPACT PROTEIN ;
10792	23825	37448	0.46	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37978	3.15	3.0E-09	BF109843.1	EST_HUMAN	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37979	3.15	3.0E-09	BF109843.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.98	2.0E-09	X16674.1	NT	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1691	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2403	15534	28661	2.24	2.0E-09	Q8Y3R5	SWISSPROT	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
4048	17204	30214	3.01	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C2TORF5 (KIAA0893)
4119	17273	30272	0.9	2.0E-09	AI263479.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5264	18363	31348	0.62	2.0E-09	M23161.1	NT	g107d09.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5837	19027	32333	0.67	2.0E-09	AI004062.1	EST_HUMAN	Human transposon-like element mRNA
6278	19452		0.75	2.0E-09	AL163249.2	NT	cl47b09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney X Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7692	20757	34242	0.66	2.0E-09	W28834.1	EST_HUMAN	z63h06.r1 Soares_testis_Nb2HFB_9W Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7971	21021	34534	0.59	2.0E-09	AI243732.1	EST_HUMAN	Alu repetitive element;
8908	21888	35528	1.2	2.0E-09	AJ271735.1	NT	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
10824	23857	37480	0.85	2.0E-09	AV698842.1	EST_HUMAN	gh88g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
12745	14013		20.06	2.0E-09	X16674.1	NT	Homo sapiens Xq pseudobulbar region; segment 1/2
12830	28188		1.86	2.0E-09	AA226070.1	EST_HUMAN	AV698842 GKC Homo sapiens cDNA clone GKCA11 5'
1019	14100		1.19	1.0E-09	W78152.1	EST_HUMAN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1133	14298	27353	1.43	1.0E-09	5031624	NT	nc11c02.r1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1133	14298	27354	1.43	1.0E-09	5031624	NT	zdf7d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346863 3' similar to gbL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
							Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
							Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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Probe SEQ ID NO.	Exon SEQ NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	15598		1.15	1.0E-09	AI359086.1	EST_HUMAN	q64e11.x1 NCJ CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element;
2854	16131	28148	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2892	16168	28184	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2892	16168	29185	6.17	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16270	29283	0.89	1.0E-09	BE635440.1	EST_HUMAN	60108802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4920	18050		6.15	1.0E-09	AA719297.1	EST_HUMAN	z335003.e1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5341	18454		0.9	1.0E-09	AA921958.1	EST_HUMAN	cm44912.e1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5620	18814	31882	0.85	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5952	19138	32454	1.29	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19446	32784	3.34	1.0E-09	P26594	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8584	21695	35206	0.92	1.0E-09	AI688474.1	EST_HUMAN	wd39605.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25t1 MER25 repetitive element;
10620	23565		2.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12842	28120	31668	1.71	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12787	25510		1.42	1.0E-09	T57366.1	EST_HUMAN	y651g12.a1 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:74758 3'
13132	26020		1.66	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14494	27564	1.62	9.0E-10	AW887740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2895	16074	29092	3.74	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL28_HUMAN P47814.60S RIBOSOMAL PROTEIN L28 ; contains element PTR5 repetitive element ; TR:O00372 O00372 PUTATIVE P150 ;
6973	20201	33627	4.98	9.0E-10	AI452982.1	EST_HUMAN	q46508.x1 Soares_NSIF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
151	13376	26408	9.28	8.0E-10	U63630.2	NT	Homo sapiens MCIM4 (MCIM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	29607	0.66	8.0E-10	BE060749.1	EST_HUMAN	QV1-BT0831-150200-071-101 BT0831 Homo sapiens cDNA
4318	17481	30446	5.45	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine 1 Homo sapiens cDNA 5' end
10170	23207		2.51	8.0E-10	U36303.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
718	13901	26942	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1651	14804	27890	2.58	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2626	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3157	16332	26341	2.25	7.0E-10	X00865.1	NT	H. sapiens DHFR gene, exon 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6514	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' and
7574	20849	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7834	20889		1.65	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF028701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF028701.2	NT	Homo sapiens presentin-1 gene, exons 1 and 2
936	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2742	15859	28971	1.03	6.0E-10	AH24405.1	EST_HUMAN	h02d07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4615	17762	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17694		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
8983	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
8983	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD62E)
9834	22874	36458	0.48	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)(ELAM-1)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2)(LECAM2) (CD62E)
780	13990		5.29	5.0E-10	AL046804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3564	16729	29745	1.14	5.0E-10	Q01033	SWISSPROT	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
5105	18233	31202	1.4	5.0E-10	AF181897.1	NT	DKFZp434N219.1 434 (synonym: hlae3) Homo sapiens cDNA clone DKFZp434N219 5'
7475	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	60182184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
114	13345		1.09	4.0E-10	AI221083.1	EST_HUMAN	Macaca tonkeana isolate 669tkpneona NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
2052	15103	28306	1.4	4.0E-10	AW594709.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2NBHP80c9W Homo sapiens cDNA clone IMAGE:1759049 3'
2640	15763	28877	6.79	4.0E-10	AL163303.2	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element; fig58g03.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
7327	20409	33871	17.76	4.0E-10	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C103
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10962	23696	37305	1.12	4.0E-10	AI267342.1	EST_HUMAN	UHH-B12-eh-a-07-9-UJ.st1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
						EST_HUMAN	ec63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035663

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-108 HT0521 Homo sapiens cDNA
939	14112	27173	2.24	3.0E-10	N36113.1	EST_HUMAN	Y632106.s1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.L1 repetitive element.
1382	14537		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4657	17793	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17793	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5350	18463	31428	0.89	3.0E-10	L34079.1	NT	Human XRCC1 DNA repair gene, genomic
5671	18767	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	Y217109.s1 Soares multiple sclerosis 2NbrHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6332	19503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
6481	19648	33010	3.82	3.0E-10	BE302870.1	EST_HUMAN	ba76608.yt NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
7637	20987	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone GBFBGD08 5'
7637	20987	34496	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone GBFBGD08 5'
8928	22007	35546	1.57	3.0E-10	H87208.1	EST_HUMAN	Y574b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element.
9249	22326	35972	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22326	35973	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22806		0.78	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10079	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	Y217102.71 Stratagene lung (4937210) Homo sapiens cDNA clone IMAGE:80398 5'
10820	23853		0.96	3.0E-10	AA769294.1	EST_HUMAN	nc36g03.s1 NCI_CGAP GC31 Homo sapiens cDNA clone IMAGE:1289908 3'
12941	25619	31977	1.87	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
38	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38	13274	26279	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1948	15089		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF675047.1	EST_HUMAN	802136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	19111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7537	20810	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	601588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34807	0.59	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8203	21285	34808	0.59	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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9502	22558		1.06	2.0E-10	BF434565.1	EST_HUMAN	7c78d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
11609	24662		1.33	2.0E-10	AI862183.1	EST_HUMAN	la10f12.x1 Soares_tctal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:20436953'
1638	14691		3.09	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-280300-001-f01 SN0038 Homo sapiens cDNA
1637	14789	27674	3.37	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXXA11 3'
2649	15772		2.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-181199-058-e08 CT0225 Homo sapiens cDNA
3589	16753	29768	0.9	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-181199-013-g10 TT0003 Homo sapiens cDNA
3629	16793		0.67	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.76	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cde
4245	17391	30378	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4245	17391	30379	16.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4285	17430		2.28	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5277	18996		1.01	1.0E-10	AI797745.1	EST_HUMAN	we2704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
7844	20713		0.58	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7860	20914	34419	0.89	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8434	21515	35046	1.14	1.0E-10	AW408990.1	EST_HUMAN	1B_6A4 Fetal brain library Homo sapiens cDNA
8855	21934		1.62	1.0E-10	AI268340.1	EST_HUMAN	qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1850874 3' similar to contains L1.11 L1 repetitive element;
10406	23441		6.24	1.0E-10	AA061888.1	EST_HUMAN	zn23g06.r1 Stralagene neuroepithelium NT2RAM1 937294 Homo sapiens cDNA clone IMAGE:548314 5'
11154	24225	37854	3.5	1.0E-10	AI038280.1	EST_HUMAN	cy65n03.x1 Soares_fetal_liver_apleer_NFLS_S1 Homo sapiens cDNA clone IMAGE:1672861 3'
12165	18503		1.8	1.0E-10	X87344.1	NT	Hi.sapiens DNA DMB, HLA-Z1, JFP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	IL2-PT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3470	16637	29658	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4622	17759	30741	0.8	9.0E-11	AA775985.1	EST_HUMAN	ac78601.s1 Stralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:370297 3'
5602	18868		3.05	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25376	32072	2.45	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-606B08 5'
3185	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yn46e03.s1 Weizmann: Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5913	19101	32416	0.66	8.0E-11	AW674316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6811	19955		0.82	8.0E-11	AW166158.1	EST_HUMAN	x448t11.x1 NCJ_CGAP_Brm60 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MIER10.L1
1479	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	MER10 repetitive element;
8695	21775	35307	2.61	7.0E-11	AF163864.1	NT	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
10434	23469		1.37	7.0E-11	P11369	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
425	13620	26661	6.19	6.0E-11	M55270.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
425	13620	26662	6.19	6.0E-11	M55270.1	NT	ENDONUCLEASE]
							Human matrix Gla protein (MGP) gene, complete cds
							Human matrix Gla protein (MGP) gene, complete cds
							Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
6862	20014	33424	0.91	6.0E-11	L44140.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7870	20924	34431	3.5	6.0E-11	P08547	SWISSPROT	AV727859 HTC Homo sapiens cDNA clone HTCCAS06 5'
8558	21640	35179	6.99	6.0E-11	AV727859.1	EST_HUMAN	CMQ-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
12	13250	26250	1	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6845	18804	35161	1.82	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7659	20764	34248	11.57	6.0E-11	11416799	NT	Homo sapiens probocadherin beta 3 (PCDH3), mRNA
1433	14586		1.39	4.0E-11	AA438042.1	EST_HUMAN	zu01b12.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2851	15985	28074	9.84	4.0E-11	BE889000.1	EST_HUMAN	601507631F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
3034	18210	29233	1.26	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17875	30858	0.87	4.0E-11	D44686.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 089
6805	19769	33154	3.29	4.0E-11	P20085	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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7141	20276	33718	0.82	4.0E-11	AA442830.1	EST_HUMAN	z68f10.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757863 5' similar to TR:G1056250 G1056250 PHEROMONE RECEPTOR VN4. ;
7532	20809		3.66	4.0E-11	AF224969.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9695	22650		1.56	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-008 HT0256 Homo sapiens cDNA f82g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WIP:ZK353.1 CE00385 ;
9862	22802	36487	0.79	4.0E-11	AI609763.1	EST_HUMAN	MRO-GN0024-180900-008-H09 GN0024 Homo sapiens cDNA
10856	23892	37513	0.94	4.0E-11	BF367283.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12794	25530	32008	1.71	4.0E-11	11545732	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
1521	14674	27756	4	3.0E-11	6679077	NT	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.3 MER10 repetitive element ;
982	14155	27215	1.43	2.0E-11	AI150502.1	EST_HUMAN	yg43e12.1f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	yg43e12.1f1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1644	14796	27880	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
1644	14796	27881	4.44	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3 beta (COR3beta) genes, complete cds
2823	15937	29047	1.09	2.0E-11	AF087013.1	NT	Human endogenous retrovirus HERV-P-T47D
3266	16440	29461	5.56	2.0E-11	P10283	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3403	16573	29568	0.92	2.0E-11	AI478617.1	EST_HUMAN	fms4c09.x1 NCI_CGAP_Kc11T Homo sapiens cDNA clone IMAGE:2101836 3'
3448	16616	29634	0.67	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
3586	16760		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3797	16958	29962	0.64	2.0E-11	P70213	SWISSPROT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
4566	17704		1.07	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-e03 BT0316 Homo sapiens cDNA
4728	17863		0.8	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21 C027
5051	18179		1.85	2.0E-11	BE062568.1	EST_HUMAN	QV2-BT0255-261039-014-e01 BT0255 Homo sapiens cDNA
5142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2- macroglobulin
6263	19437	32784	1.23	2.0E-11	AW877808.1	EST_HUMAN	QV2-P10073-280300-109-P09 PT10073 Homo sapiens cDNA

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6440	19607	32970	2	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCL_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR10_YEAST
7345	20425	33888	0.85	2.0E-11	BF592945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.1
8066	21148		0.59	2.0E-11	P37072	SWISSPROT	787603.x1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:3442565 3'
9424	22498		1.39	2.0E-11	AF029308.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
10491	23526	37135	5.13	2.0E-11	Q13605	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10734	23767	37376	1.09	2.0E-11	AW885874.1	EST_HUMAN	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24438	38084	1.84	2.0E-11	AA035369.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24438	38085	1.84	2.0E-11	AA035369.1	EST_HUMAN	Zk27602.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
11408	24469	38133	1.4	2.0E-11	AA261856.1	EST_HUMAN	Zk27602.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
12122	25102	38807	12.19	2.0E-11	AL163278.2	NT	Zs18804.r1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
12287	28105		1.85	2.0E-11	AA704195.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12328	25237		1.44	2.0E-11	AW842143.1	EST_HUMAN	Z177603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12354	25256	32115	2.15	2.0E-11	BF37869.1	EST_HUMAN	RC0-CN0027-210100-071-c01 CN0027 Homo sapiens cDNA
12641	25431		1.43	2.0E-11	D25217.2	NT	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12813	25642		3.82	2.0E-11	P08547	SWISSPROT	Homo sapiens mRNA for KIAA0027 protein, partial cds
13180	25767		2.5	2.0E-11	11417968	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
683	13678	28909	1.57	1.0E-11	AJ131016.1	NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA
809	13686	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens SCL gene locus
1244	14403	27484	2.91	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C009
1528	14881		1.82	1.0E-11	AF110914.1	NT	Homo sapiens chromosome 21 segment HS21C079
2095	15235	28356	0.94	1.0E-11	P16258	SWISSPROT	Homo sapiens PRO3078 mRNA, complete cds
2195	15330	28455	3.59	1.0E-11	AF000573.1	NT	OXYSTEROL-BINDING PROTEIN
2229	15363	28492	1.1	1.0E-11	AA309918.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3588	16752	29767	0.95	1.0E-11	BE004315.1	EST_HUMAN	EST:180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5447	18647	31625	14.68	1.0E-11	AL163247.2	NT	CMD-BN0106-170300-292-d12 BN0106 Homo sapiens cDNA
5953	19139	32455	0.78	1.0E-11	BF222846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
8398	21477	35004	2.85	1.0E-11	4885546	NT	7p57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.b3
8781	21860	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	MER10 repetitive element
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
							Y73008.r1 Soares_infant_brain_1N18 Homo sapiens cDNA clone IMAGE:28166 5'
							QV4-NN1148-250900-423-a03 NN1148 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9248	22325	35871	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
10626	23660		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	1.0E-11	BF880078.1	EST_HUMAN	602184807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4298977 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADH.P_Human fetal Brain Whole tissue Homo sapiens cDNA
3017	16193	29218	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	22604		0.89	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12408	25287		4.68	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4783	17918	30905	1.57	7.0E-12	Q05904	SWISSPROT	34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	Z23901.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25933		1.18	7.0E-12	D19473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.95	8.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW706 5'
4488	17608	30586	9.23	8.0E-12	AA732516.1	EST_HUMAN	nz8811.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
5336	18449	31418	5.12	8.0E-12	AI459181.1	EST_HUMAN	ij65g12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2146438 3' similar to contains MER10.12 MER10 MER10 repetitive element;
9196	22274	35911	1.09	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9676	22637		1.81	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367889 similar to contains MER29.12 MER29 repetitive element;
13205	25786		1.25	6.0E-12	AW886846.1	EST_HUMAN	RC4-OT0072-080400-012-11 OT0072 Homo sapiens cDNA
1068	14234	27293	2.37	5.0E-12	T06673.1	EST_HUMAN	EST04462 Fetal brain, Striagena (cat#636206) Homo sapiens cDNA clone HFBDV33
3477	16644	29663	1.28	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
3821	16981	29984	7.44	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32686	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32667	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19780	33168	9.96	5.0E-12	AW974760.1	EST_HUMAN	EST386850 MAGe resequences; MAGN Homo sapiens cDNA
7176	20052	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21505	35038	1.28	5.0E-12	AA033745.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8867	21946		0.55	6.0E-12	AW887037.1	EST_HUMAN	RC1-OT0086-220300-011-507 OT0086 Homo sapiens cDNA
9195	22273		0.77	6.0E-12	AL079581.1	EST_HUMAN	DKFZp434J0426.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
9308	22384	35036	2.52	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9923	22879	36247	1.22	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.89	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10763	23828	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	26505	3.29	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
255	13474	26505	3.42	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:460678 3'
4742	17877	30860	0.88	4.0E-12	AI688984.1	EST_HUMAN	bx2h05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13639 Q13639
7797	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	MARINER TRANSPOSASE. ; nad21b03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element. ;
8437	21518		4.81	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PST and hypothetical protein genes, complete cds; and S171 gene, partial cds
11338	24401	38050	4.33	4.0E-12	AJ229043.1	NT	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12684	25466		2.11	4.0E-12	U78027.1	NT	Homo sapiens Bruin's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13818	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
631	13816	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
5276	18395	31363	0.78	3.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8570	21651	35193	0.5	3.0E-12	O38453	SWISSPROT	SERINE PROTEASE HEPSPIN
10891	23975	37605	2.32	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27921	1.24	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3556	16721	29736	0.93	2.0E-12	AW802131.1	EST_HUMAN	IL5-JM0071-120400-065-e05 UM0071 Homo sapiens cDNA
4230	17377	30365	1.29	2.0E-12	J01894.1	NT	Nus musculus keratin-associated protein 8.2 (Krtap8-2), mRNA
4230	17377	30366	1.29	2.0E-12	J01894.1	NT	Rat Uga small nuclear RNA
4541	17678		2.03	2.0E-12	BE083609.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	TEX15 PROTEIN (T-BOX PROTEIN 15)
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TEX15 PROTEIN (T-BOX PROTEIN 15)
6606	18766		2.08	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGC sequences, MAGL Homo sapiens cDNA
7326	20408	33670	3.85	2.0E-12	T08199.1	EST_HUMAN	EST06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559:200400-016-e08 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10191	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.76	2.0E-12	AI334130.1	EST_HUMAN	q407602.x1 Soares_NhlMfu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
12129	25109	38813	1.53	2.0E-12	AW242334.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN. ;
12313	25228		1.34	2.0E-12	AL163283.2	NT	xn27403.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694965 3'
12516	25352		1.46	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
125	13354	28385	1.64	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2044	15185		1.78	1.0E-12	AI871728.1	EST_HUMAN	hm90409.x1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
3138	16314	28326	1.04	1.0E-12	AF000991.1	NT	hm51f07.x1 NCJ_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.53 L1
3138	16314	28327	1.04	1.0E-12	AF000991.1	NT	repetitive element ;
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6088	19269		1.6	1.0E-12	U82828.1	NT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' ~
6186	19342		1.82	1.0E-12	Q872G7	SWISSPROT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' ~
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6282	19455	32808	0.59	1.0E-12	BF642800.1	EST_HUMAN	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6662	19821	33208	0.63	1.0E-12	AF229843.1	NT	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
7265	20348	33900	2.53	1.0E-12	AF198864.1	NT	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
7300	20382	33840	10.78	1.0E-12	A1248533.1	EST_HUMAN	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7300	20382	33841	10.78	1.0E-12	A1248533.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							q466a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;
							q466a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:U19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8686	21768	35298	0.59	1.0E-12	U68059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P1, TCRBV7S2A1N4T, TCRBV13S9/13S>
8802	21981	35521	1.26	1.0E-12	AA782323.1	EST_HUMAN	ac28d05.s1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25168	38835	2.32	1.0E-12	AW062164.1	EST_HUMAN	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
12437	25310		1.54	1.0E-12	AI738592.1	EST_HUMAN	w33h08.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2392085 3'
12600	26068		1.93	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12788	26168		1.19	1.0E-12	P44838	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR H10712 PRECURSOR
12951	26861		2.82	1.0E-12	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4056	17212	30223	1.21	9.0E-13	AB029300.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9801	22841		2.81	9.0E-13	N69853.1	EST_HUMAN	za26b06.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:293651 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	15029	28136	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34906	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCL_CGAP_UK Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCL_CGAP_UK Homo sapiens cDNA clone IMAGE:2437601 3'
10350	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21510		0.77	7.0E-13	Q96166	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3868613 6'
12978	26835		1.63	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2168	15303	28430	5.65	6.0E-13	AL16207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5239	16367	31329	0.93	6.0E-13	AI267928.1	EST_HUMAN	q64409.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1911352 3'
3398	16569		1.15	6.0E-13	R78338.1	EST_HUMAN	y82104.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:145759 5'
3484	16652		1.56	5.0E-13	AA435773.1	EST_HUMAN	z17a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728360 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
7016	20152	33572	0.99	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11100	24173	37808	2.84	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1916	15059		4.88	4.0E-13	AW37861.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15856		1.61	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4869	18002		1.06	4.0E-13	AA454054.1	EST_HUMAN	z46d07.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5704	18997	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7356	20434	33696	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	z476g12.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7896	20950		2.62	4.0E-13	N44291.1	EST_HUMAN	Y33g05.r1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32895
9042	22121	35663	1.38	4.0E-13	AL049810.1	EST_HUMAN	A32895 t complex sterility protein - mouse
9702	22751	36821	0.47	4.0E-13	AA076907.1	EST_HUMAN	DKFZp434A0128.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
10226	23262	36850	4.44	4.0E-13	AL289831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	q32d05.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	z476g10.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
184	13408		4.35	3.0E-13	AF003528.1	NT	z476g10.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1502	14855	27737	0.96	3.0E-13	AL904151.1	EST_HUMAN	z46d08.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2443	15571	28700	1.53	3.0E-13	AL271736.1	NT	GM-BT043-090299-075 BT043 Homo sapiens cDNA
2648	16673		2.28	3.0E-13	AL163210.2	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2729	15847	28957	3.69	3.0E-13	BF372982.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	GM3-F10100-140700-242-008 F10100 Homo sapiens cDNA
3592	16756	29771	9.73	3.0E-13	P18616	SWISSPROT	z46d02.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5657	18851	32133	0.68	3.0E-13	AA134017.1	EST_HUMAN	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5657	18851	32134	0.88	3.0E-13	AA134017.1	EST_HUMAN	z46d10.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element
6114	19294	32629	0.73	3.0E-13	AW005639.1	EST_HUMAN	z46d02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
8067	21149	34869	7.1	3.0E-13	U52111.2	NT	O75139 KIAA0644 PROTEIN ; Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8288	21350	34885	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to serine protease P100, Ra-reactive factor
8288	21350	34886	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to serine protease P100, Ra-reactive factor
10401	23436	37043	0.58	3.0E-13	AW595487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23998		3.1	3.0E-13	AJ064768.1	EST_HUMAN	HA0636 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE063509.1	EST_HUMAN	CN0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
11898	24888	38585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
154	13379	28411					Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	28502	2.06	2.0E-13	U52111.2	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1289	14465	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POL.D2) gene, exons 1 through 11 and complete cds
3070	18246	29268	0.81	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	18246	29287	0.81	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3588	16760	28776	1.88	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19508		0.58	2.0E-13	X79417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6954	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKFB gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7189	20084	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7189	20084	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10875	23709	37917	2.41	2.0E-13	5031886	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12388	25274		22.49	2.0E-13	AW892155.1	EST_HUMAN	CN0-NIN0001-100300-274-e11 NN0001 Homo sapiens cDNA
302	13518	28551	1.34	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14088	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1387	14521	27596	1.4	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, ILP2, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2078	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element:
4715	17850	30833	1.32	1.0E-13	BF340987.1	EST_HUMAN	602038005F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:418588 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8084	21176	34691	0.97	1.0E-13	AA577812.1	EST_HUMAN	m24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8084	21176	34692	0.97	1.0E-13	AA577812.1	EST_HUMAN	m24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10285	23330		1.04	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10508	23543	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11681	24740	38431	0.74	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12206	25160		1.38	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12920	25005		3.46	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13077	25706		1.85	1.0E-13	X87578.1	NT	H.sapiens CD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2559	15594		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	29036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	29360	7.5	9.0E-14	AW513286.1	EST_HUMAN	xc54p05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	a24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3698	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	18010	30994	2.23	9.0E-14	AJ002153.1	NT	Sequinius oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4088	17222		3.64	8.0E-14	R76289.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9647	21090	34605	38.93	8.0E-14	X8921.1	NT	H.sapiens DNA for endogenous retroviral like element
9760	22888	36286	3.22	8.0E-14	AA219310.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11717	24757		1.79	8.0E-14	BE062658.1	EST_HUMAN	QV2-B.T0258-261099-014-a01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	A1688118.1	EST_HUMAN	wc2108.x1 NCI_CGAP_C33 Homo sapiens cDNA clone IMAGE:2328143 3'
1858	18044		4.78	7.0E-14	AW151673.1	EST_HUMAN	x167e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9120	22189		0.73	7.0E-14	AL163285.2	NT	MER10 repetitive element;
378	13596	26620	12.43	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
							Homo sapiens FRA3B common fragile region, diadenosine triphosphatase (FHT) gene, exon 5

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10027	23066	36682	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10027	23065	36683	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
633	13818	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5166	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	X00305.x1 NCL CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575186 3' similar to contains L1.12 L1 repetitive element.
5650	18544	32125	5.26	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	18030		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1926	15089	28174	10.15	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	AA046502.1	EST_HUMAN	Zk67408.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4407	17549	30633	1.04	4.0E-14	N46328.1	EST_HUMAN	Y73c12.e1 Soares_multiple_sclerosis_ZNBHMS Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element.
8145	21227		0.71	4.0E-14	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12043	25024	38720	5.5	4.0E-14	BE242468.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470
12966	26203		5.69	4.0E-14	AJ886224.1	EST_HUMAN	wm08c03.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element.
972	14145	27204	1.50	3.0E-14	X98488.1	NT	R.norvegicus mRNA for CP-G2 protein
6873	20025	33434	0.93	3.0E-14	A420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
6873	20025	33435	0.93	3.0E-14	A420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2084070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
7173	20306	33749	0.6	3.0E-14	A4388311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
6987	22095	35606	0.86	3.0E-14	N42185.1	EST_HUMAN	Y07610.1 Soares_melanocyte_ZNBHM Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER39 repetitive element.
11612	18465	31533	5.87	3.0E-14	AW265354.1	EST_HUMAN	X04512.x1 NCL CGAP_H11 Homo sapiens cDNA clone IMAGE:270523 5'
12804	26041		1.88	3.0E-14	AL169285.2	NT	Homo sapiens chromosome 21 segment HS21C085
13212	25694	31853	1.51	3.0E-14	BE891550.1	EST_HUMAN	601435233.F1 NH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'
401	13598	28634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
401	13598	28635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
708	16019	28925	11.36	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2467	15588		1.04	2.0E-14	AW372888.1	EST_HUMAN	RC6-BT0377-091289-031-D12 5T0377 Homo sapiens cDNA
2535	15690		0.99	2.0E-14	7657526	NT	Homo sapiens thaboid tumor deletion region protein 1 (RTDR1), mRNA
2593	15718	28835	1.53	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31912	0.97	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	AI312351.1	EST_HUMAN	ta7801.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20159		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.46	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.56	2.0E-14	AI978795.1	EST_HUMAN	wr59g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23664	37273	0.51	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBF04.6
11019	24038	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B1-adv-a-10-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15680		1.26	2.0E-14	7657526	NT	Homo sapiens thaboid tumor deletion region protein 1 (RTDR1), mRNA
1092	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14551	27664	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27665	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	15198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from flamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001889.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0492-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0492-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30155	1.69	1.0E-14	AA682984.1	EST_HUMAN	ae89c12.s1 StrataGene echizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733	30713	2.01	1.0E-14	AW276852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
							Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5930	19116	32429	1.98	1.0E-14	AF126145.1	NT	mitochondrial protein, complete cds
6813	26834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse) like 1 (PROM1), mRNA
6813	26834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse) like 1 (PROM1), mRNA
1607	14790	27839	1.81	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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2242	16376		1.38	9.0E-15	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α s
7663	20732	34207	4.24	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P16, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE903559.1	EST_HUMAN	001677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980159 5'
13099	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE281482.1	EST_HUMAN	607148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	BF035327.1	EST_HUMAN	607455531F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23684		2.34	7.0E-15	AW241958.1	EST_HUMAN	0077402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.12 THR repetitive element ;
12270	25203		1.44	7.0E-15	AA284485.1	EST_HUMAN	zs57408.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb:L21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.11 L1 repetitive element ;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5263	18382		0.98	6.0E-15	AW901258.1	EST_HUMAN	GM4NN1011-100300-110-310 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
11583	26231		1.54	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13018	26858	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2818	15833	28044	1.76	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	P11359	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
440	13240	26240	2.33	4.0E-15	AL163303.2	NT	ENDONUCLEASE]
6804	18859	33359	0.9	4.0E-15	AB007870.1	NT	Homo sapiens chromosome 21 segment HS21C103
11316	21065	34577	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34676	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.67	3.0E-15	N89452.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
5141	18264	31232	0.67	3.0E-15	AA078097.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANFCARDIODILATIN)
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6853	20280		1.11	3.0E-15	Q84625	SWISSPROT	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7430	20507	33978	3.13	3.0E-15	M27695.1	NT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33979	3.13	3.0E-15	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20507	33979	3.13	3.0E-15	M27695.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10129	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element ;
11033	24112	37748	8.11	3.0E-15	AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
260	13479	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1569	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17980		2.76	2.0E-15	AI806335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR.Q61043 Q61043 NINEIN ;
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	801344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	801344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7263	20346		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20493	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	zi77603.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7554	20626	34102	5.05	2.0E-15	W05064.1	EST_HUMAN	za78d10.r1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9107	22186	35730	2.86	2.0E-15	D14547.1	NT	WP.F44F4.B CE02227 TRANSPOSASE ;
9273	22349	35899	0.91	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9273	22349	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	zi77608.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9804	22659	36231	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9804	22659	36232	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11077	24162		3.69	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13018	16763	28779	3.89	2.0E-16	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15948		3.09	1.0E-15	AI689984.1	EST_HUMAN	b23h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
3077	16283	28278	1.42	1.0E-15	BE043584.1	EST_HUMAN	MARINER TRANSPOSASE. ;
3211	16355	29396	1.18	1.0E-15	P08547	SWISSPROT	tk40602.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
4479	17619	30601	0.61	1.0E-15	BE182696.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6502	19668	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	RC3-H10849-100500-022-508 H10849 Homo sapiens cDNA
7149	20284		1.98	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7184	20049	33480	0.79	1.0E-15	P39057	SWISSPROT	QV3-BT0566-270100-074-g05 BT0569 Homo sapiens cDNA
8427	21508	35040	0.99	1.0E-15	AI163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8616	21696	35232	4.94	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35233	4.94	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8238	22316	35858	0.78	1.0E-15	AL163207.2	NT	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9242	22319	35862	0.96	1.0E-15	4607208	NT	Homo sapiens chromosome 21 segment HS21C007
9448	22564	36127	0.89	1.0E-15	Q39575	SWISSPROT	Homo sapiens spermidine synthase (SRM) mRNA
9832	22872	36455	0.94	1.0E-15	AA864653.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
11057	24134	37770	3.04	1.0E-15	AF044083.1	NT	ch37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1499872 3' similar to contains L1: k3 L1 repetitive element ;
13104	25892	31856	13.05	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4626	17762	30744	0.83	9.0E-16	4503168	NT	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element;
11241	24310	37947	1.41	9.0E-16	P08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
11895	24980	36685	1.48	9.0E-16	A1244341.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11995	24980	36686	1.48	9.0E-16	A1244341.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.k3
5819	19009	32315	0.85	7.0E-16	4858120	EST_HUMAN	MER10 repetitive element ;
7496	20571	34043	1.3	7.0E-16	O88807	SWISSPROT	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.k3
7496	20571	34044	1.3	7.0E-16	O88807	SWISSPROT	MER10 repetitive element ;
13043	25995		38.08	7.0E-16	T94149.1	EST_HUMAN	Homo sapiens chordin (C-C motif) receptor 8 (CGR8) mRNA
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							ye28c12.11 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:118082 5'

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2208	15342		9.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1522	14976	27757	0.96	5.0E-16	AJ251154.1	NT	Mus musculus ciliary receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA992178.1	EST_HUMAN	cd80-c04.s1 Soares, total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11809	24799	38498	2.68	5.0E-16	BF217368.1	EST_HUMAN	contains element L1 repetitive element;
13152	25749		14.15	5.0E-16	11418127	NT	601885734FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2463	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2463	15581	28709	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3546	18711	29722	5.29	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30391	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4260	17405	30392	8.68	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	IP08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	36114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12393	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.68	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12382	25277	32079	3.23	4.0E-16	6912469	EST_HUMAN	Homo sapiens Gp2-associated binder 2 (KIA00571), mRNA
12692	25454		1.33	4.0E-16	R18591.1	NT	y96511.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	dl45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
135	13361	26396	1.09	3.0E-16	AW022862.1	EST_HUMAN	dl45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13673		1.58	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13682		2.33	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14636	27720	2.73	3.0E-16	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
3041	16217	29237	4.71	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4711	17846	30830	0.59	3.0E-16	AW160828.1	EST_HUMAN	au76b06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to
5057	18185	31160	1.32	3.0E-16	AV661933.1	EST_HUMAN	SW-KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5392	18594		0.99	3.0E-16	AA077225.1	EST_HUMAN	AV661383 GLC Homo sapiens cDNA clone GLC3SA01 3'
5734	18927	32223	1.67	3.0E-16	AF003529.1	NT	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
8858	21937	35473	4.25	3.0E-16	AL002836.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
							am98h05.s1 Stratagene echino brain S11 Homo sapiens cDNA clone IMAGE:1664185 3' similar to contains
							THRLb2 THR repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36969	2.59	3.0E-16	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	28171	31557	3.62	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L1623 5'
994	14168		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2459	15583		0.96	2.0E-16	AA621761.1	EST_HUMAN	af06004.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2753	15870		1.14	2.0E-16	J03061.1	EST_HUMAN	Human SSAV-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	AI208733.1	EST_HUMAN	q55603.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
5299	18416	31385	0.84	2.0E-16	BE061178.1	EST_HUMAN	MER29 repetitive element;
6880	20032	33442	0.68	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-131189-003-H12 BT0048 Homo sapiens cDNA
7893	20945	34451	0.99	2.0E-16	AI470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							g16e11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
8154	21236	34757	1.67	2.0E-16	AI732837.1	EST_HUMAN	nz4708.x5 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849
8352	21433	34957	0.81	2.0E-16	BE88026.1	EST_HUMAN	HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905; contains MER7.11 MER7 repetitive element;
8352	21433	34958	0.81	2.0E-16	BE88026.1	EST_HUMAN	782f09.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.78	2.0E-16	AW877214.1	EST_HUMAN	782f09.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35341	0.78	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	AF200719.1	NT	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
363	13630		22.93	1.0E-16	AA628592.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
2028	15169	28276	3.42	1.0E-16	BF327942.1	EST_HUMAN	af39p11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1034094 3' similar to
5839	19029	32335	0.6	1.0E-16	AF163864.1	NT	contains ORF.12 ORF repetitive element;
6565	19727		18	1.0E-16	U45883.1	NT	QV0-BN0148-070700-293-at0 BN0148 Homo sapiens cDNA
8704	19882	33252	2.86	1.0E-16	Q02779	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7726	19727		5.39	1.0E-16	U45883.1	NT	Homo sapiens COR8 chemokine receptor (CXCR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875651.1	EST_HUMAN	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
3832	16992	28994	2.08	9.0E-17	AW900048.1	EST_HUMAN	Homo sapiens COR8 chemokine receptor (CXCR8) gene, complete cds
6864	20016		2.15	9.0E-17	AI392964.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
							CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
							ig22c11.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
							MER28 repetitive element;

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8299	21381		3.58	9.0E-17	AW160257.1	EST_HUMAN	xg49g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element ;
10428	23464		2.35	8.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3998	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5701	25909	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone H1FAQB07 5'
1487	14940		2.58	7.0E-17	8753097	NT	Mus musculus adiponectin B editing complex 2 (Apobec2), mRNA
5438	18638		3.11	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6826	19979	33387	7.91	7.0E-17	AF228943.1	NT	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
208	13431	26463	5.62	6.0E-17	AW993880.1	EST_HUMAN	H81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element ;
6443	19810	32973	2.05	6.0E-17	AW662772.1	EST_HUMAN	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
10499	23634	37144	0.54	6.0E-17	P20138	SWISSPROT	yc05h08.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
434	13234	26234	2.37	5.0E-17	T64110.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
7759	20818	34308	1.81	6.0E-17	T81043.1	EST_HUMAN	x20c04.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element ;
9562	22704	36270	1.32	4.0E-17	AW129165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11783	24773	38469	2.51	4.0E-17	AL163247.2	NT	QV45604.x1 Soares_Testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 O16530 PMS3 MRNA; contains MER10.12 MER10 repetitive element ;
12308	25226		1.82	4.0E-17	A073546.1	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
2165	15300	28426	1.85	3.0E-17	AW119123.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3283	16437		1.17	3.0E-17	P35410	SWISSPROT	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181998 3'
3732	16893	29897	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181998 3'
3732	16893	29898	1.91	3.0E-17	BE326522.1	EST_HUMAN	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element ;
8463	21544	35074	1.12	3.0E-17	N68451.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9903	22843	36528	5.19	3.0E-17	AB026898.1	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
12268	25201		4.2	3.0E-17	11417968	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13155	28761		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLODIF08 5'
363	13574	26605	2.65	2.0E-17	AI270080.1	EST_HUMAN	qf83a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element
364	13574	26605	2.78	2.0E-17	AI270080.1	EST_HUMAN	qf83a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA72832.1	EST_HUMAN	Zg81404.s1 Scores fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2518	15644	28765	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2518	15644	28766	2.59	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2988	16172	28101	6.96	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31698	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31697	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19563		1.92	2.0E-17	AF030066.1	NT	Homo sapiens MHC class 1 region
6619	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610.r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8006	21056	34568	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KAA1418 protein, partial cds
8276	21367	34875	1.24	2.0E-17	Q85156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10073	23111	36715	2.71	2.0E-17	BE269888.1	EST_HUMAN	600844690.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880615 5'
10108	23146	36744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23146	36745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10466	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10580	23625	37232	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10580	23625	37233	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.93	2.0E-17	A1798902.1	EST_HUMAN	w694b04.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23652	37262	0.93	2.0E-17	A1798902.1	EST_HUMAN	w694b04.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	13950	26999	2.79	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1807	14956	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542	28689	3.16	1.0E-17	U78410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3667	16820		1.03	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4266	17401		9.42	1.0E-17	R08942.1	EST_HUMAN	y30a07.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128388 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6781	19946	33344	1.62	1.0E-17	AI185642.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6791	19946	33346	1.62	1.0E-17	AI185642.1	EST_HUMAN	qe55b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33766	1.33	1.0E-17	Q19831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPAE)
8792	21871	35410	1.26	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0283-101299-072-007 BT0283 Homo sapiens cDNA
10210	23246	36836	1.04	1.0E-17	AW998538.1	EST_HUMAN	QV3-BN0046-220300-128-c10 BN0046 Homo sapiens cDNA
11703	24700	38393	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747		3.05	9.0E-18	AI472167.1	EST_HUMAN	ly85d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3886	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNST) mRNA
359	13570	26599	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCLCGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7601	20871	34145	1.09	7.0E-18	AW887542.1	EST_HUMAN	RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA
12826	13570	26599	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCLCGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12826	13570	26600	10.65	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3387	16539	29552	1.23	6.0E-18	X71791.2	NT	Rattus norvegicus partial GdnRn-1 gene for glia-derived nexin/protease nexin 1, enhancer region
4888	18001		3.99	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8444	21925		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8543	21824	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	AI808256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	AI908256.1	EST_HUMAN	RC-BT166-020499-014 BT166 Homo sapiens cDNA
11399	24460	38124	3.63	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24664	38351	1.69	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12634	25364	32068	3.91	6.0E-18	U87929.1	NT	Human acornate hydratase (ACO2) gene, exon 4
1171	14334	27390	12.48	5.0E-18	AI280214.1	EST_HUMAN	qm85g11.x1 Soares_placenta_8to8weeks_2NbHP8to8W Homo sapiens cDNA clone IMAGE:1893668 3'
4433	17573	30555	0.59	5.0E-18	10946655	NT	similar to contains Alu repetitive element,
5387	18589	31561	1.23	5.0E-18	AF087913.1	NT	Mus musculus gasdermin (Gsdm), mRNA
8917	21996	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-147D
							NR0-HTT0161-221099-002-c06 HTT0161 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37932	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC61088), mRNA
11223	24292	37933	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC61088), mRNA
12875	25450		6.28	5.0E-18	AW867182.1	EST_HUMAN	MIR1-SNO035-060400-001-g11 SNO035 Homo sapiens cDNA
13063	25698		28.96	5.0E-18	AV850547.1	EST_HUMAN	AV850547 GLC Homo sapiens cDNA clone GLCCGA02 3'
127	13355	26396	0.91	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1754	14903	27996	52.62	4.0E-18	AA621814.1	EST_HUMAN	h036h04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26328
1038	15081		1.05	4.0E-18	A1738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2274	15407	28536	1.26	4.0E-18	Q08430	SWISSPROT	w133103.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2274	15407	28537	1.26	4.0E-18	Q08430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (H-BRANCHING ENZYME) (IGNT)
3892	17051	30050	0.61	4.0E-18	A1581586.1	EST_HUMAN	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (H-BRANCHING ENZYME) (IGNT)
5478	18678	31691	2.47	4.0E-18	A1017595.1	EST_HUMAN	ACETYL GLUCOSAMINYL TRANSFERASE (H-BRANCHING ENZYME) (IGNT)
5478	18678	31692	2.47	4.0E-18	A1017595.1	EST_HUMAN	ACETYL GLUCOSAMINYL TRANSFERASE (H-BRANCHING ENZYME) (IGNT)
8029	21112		0.92	4.0E-18	AA746811.1	EST_HUMAN	ar83b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains ALU repetitive element;
11254	24323	37984	7.59	4.0E-18	AA371807.1	EST_HUMAN	EST containing O family repeat
872	14048	27114	3.81	3.0E-18	AA814186.1	EST_HUMAN	EST83633 Pituitary gland, subtraced (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to
963	14128	27187	2.25	3.0E-18	BE088834.1	EST_HUMAN	cb23h11.1 NCL_CGAP_K45 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
4060	17216	30226	1.06	3.0E-18	AL163247.2	NT	P45762 40S RIBOSOMAL PROTEIN S6;
6968	20198	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	CM0-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
11167	24238	37869	1.99	3.0E-18	BF218650.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12832	25564		4.56	3.0E-18	AW022015.1	EST_HUMAN	PMO-BN0081-100300-001-508 BN0081 Homo sapiens cDNA
261	13460	26512	4.2	2.0E-18	BE256097.1	EST_HUMAN	60184856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103662 5'
1176	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	df31h12.y1 Morbin Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
3193	16368	29374	0.94	2.0E-18	Q39575	SWISSPROT	GV1-L10038-150200-070-907 L10036 Homo sapiens cDNA
							60114362F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA868610.1	EST_HUMAN	ak63a07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:O14577
5623	18817	31886	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5889	19184		1.64	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6294	19467	32820	0.91	2.0E-18	X60456.1	NT	602021164F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
6294	19467	32821	0.91	2.0E-18	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32938	0.9	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6448	19615	32979	2.93	2.0E-18	AW665893.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7594	20665	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	h94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979684 3' similar to contains
8341	21422	34947	0.5	2.0E-18	BE439524.1	EST_HUMAN	MER19.12 MER19 repetitive element;
10253	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	ea89d11.r1 Striatagens fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
10253	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12031	25014	38716	4.46	2.0E-18	AW151299.1	EST_HUMAN	MER10 repetitive element;
12465	14339		12.67	2.0E-18	BE286097.1	EST_HUMAN	x67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
4537	17875		0.76	1.0E-18	T85408.1	EST_HUMAN	MER10 repetitive element;
5471	18871	31651	2.64	1.0E-18	AV653405.1	EST_HUMAN	x67e10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	MER8 repetitive element;
5688	18882	32175	3.08	1.0E-18	D00099.1	NT	801114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5584	19746	33128	1.31	1.0E-18	AL163280.2	NT	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains
5937	21717	35254	1.05	1.0E-18	AI148288.1	EST_HUMAN	L1 repetitive element;
10103	25141	36740	4.93	1.0E-18	U91328.1	NT	L1 repetitive element;
12416	25294	32084	4.65	1.0E-18	AF003528.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
560	13762	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8032	21115		3.69	9.0E-19	F08688.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8886	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21965	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24463	38116	3.15	9.0E-19	AB032959.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13762	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1073	14239		1.58	8.0E-19	AW974902.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158936.1	EST_HUMAN	MFO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
2319	15451	26583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6886	19747	33129	2.11	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P26444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	A1344951.1	EST_HUMAN	fb01c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	28183		1.72	7.0E-19	AA705684.1	EST_HUMAN	z6b001.s1 Soares_fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3879	17038		1.16	6.0E-19	AW852930.1	EST_HUMAN	PMO-CT0248-131059-001-g01 CT0248 Homo sapiens cDNA
4585	17722	30706	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5978	19163	32483	5.17	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR [ZONA PELLUCIDA GLYCOPROTEIN ZP-X] (RC56)
6346	18516	32873	0.59	5.0E-19	AW663302.1	EST_HUMAN	hh7706.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	23673	37283	1.18	5.0E-19	AJ297899.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38509	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element: MSR1 repetitive element;
13083	25895		1.34	5.0E-19	U66090.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S9P, TCRBV6S9A1N1T, TCRBV6S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
568	13760	26784	0.96	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15884	28975	1.15	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17643	30529	0.55	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4400	17643	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4969	17707	30686	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADG Homo sapiens cDNA clone ADCAMA11 5'
5394	18696		0.69	3.0E-19	AF223497.1	NT	Homo sapiens NP0008 protein (NP0008) mRNA, complete cds
7543	20615		1.88	3.0E-19	1143221.4	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
9658	21101	34614	1.09	3.0E-19	X69695.1	NT	M.musculus mRNA for TPCR33 protein
12563	25385		16.36	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PB1) mRNA, complete cds
2627	19750	28865	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4568	17706		1.34	2.0E-19	AI311783.1	EST_HUMAN	qo81602.X1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1915698 3' similar to TR:Q66386 Q66386 POL/ENV GENE;
6179	19355	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20558	34040	0.63	2.0E-19	7687286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8525	21606	35145	10.24	2.0E-19	AA012854.1	EST_HUMAN	z63409.7.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36763	0.84	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
484	13689		1.86	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2233	15367	28496	1.64	1.0E-19	H30795.1	EST_HUMAN	yo7907.7.1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2782	15998		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2906	16087		6.72	1.0E-19	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16655	29869	1.18	1.0E-19	AA834967.1	EST_HUMAN	449b12.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1383631 3' similar to contains MER37.12 MER37 repetitive element;
6452	18652	31631	0.73	1.0E-19	AI890865.1	EST_HUMAN	wm91b08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16630 Q16630 PMS3 mRNA;
6199	19374	32725	2.6	1.0E-19	U12186.1	NT	Oryzias latipes sodium/dicarboxylate cotransporter mRNA, partial cds
6337	26213		0.63	1.0E-19	AA595627.1	EST_HUMAN	rh22403.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:983093 similar to contains L1.1 L1 repetitive element;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryzias latipes Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	Oryzias latipes Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25956		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21724	35261	1.94	1.0E-19	M84657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
8839	22018		2.72	1.0E-19	T98920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
8950	22959		0.69	1.0E-19	U90822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23425	37032	25.12	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	Y91609.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37888	1.87	1.0E-19	BE616026.1	EST_HUMAN	601279892FT NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3811463 5'
6784	18939	33336	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Ktap9-1), mRNA
6784	19939	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Ktap9-1), mRNA
7687	20752	34234	1.46	8.0E-20	AI221371.1	EST_HUMAN	qg86109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34235	1.46	8.0E-20	AI221371.1	EST_HUMAN	qg86109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	18521	29537	0.71	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0068-050900-003-at4 AN0068 Homo sapiens cDNA
7134	18550	31474	5.65	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092.r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	n46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	n46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
12014	24958		2.89	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13a), mRNA
3845	18808	29822	3.64	6.0E-20	P30188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4387	17530	30511	4.58	6.0E-20	BE822434.1	EST_HUMAN	601441231FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
7284	20347	33789	1.42	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HAO250
8131	21213	34733	6.96	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8131	21213	34734	6.96	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8295	21377	34898	0.79	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9035	22114	35657	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9035	22114	35658	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9044	21087		1.13	5.0E-20	O60609	SWISSPROT	HYPOTHETICAL PROTEIN DJ849024.1
1849	14802	27889	0.94	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5785	18967		1.13	4.0E-20	O89980	SWISSPROT	HISTONE H2B C (H2B/C)
8110	21192		5.61	4.0E-20	AI874352.1	EST_HUMAN	1264903.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2293396 3'
10717	23750	37357	1.13	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17468	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4747	17882	30864	1.08	3.0E-20	AA037818.1	EST_HUMAN	Zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1 L3 L1 repetitive element;
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10527	23562	37168	0.47	3.0E-20	BF185264.1	EST_HUMAN	601843561FT NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12331	25239	32109	6.09	3.0E-20	BE888422.1	EST_HUMAN	601514180FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915622 5'
853	14030		5.65	2.0E-20	AW303888.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RSS_MOUSE
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lj2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN.;
2878	14030		5.32	2.0E-20	AW303888.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
5061	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN.;
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	P97461_40S RIBOSOMAL PROTEIN S5.;
5256	18376		0.9	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
9309	21391	34915	0.97	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens melate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9391	22456	36030	2.65	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
9391	22456	36031	2.65	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12743	25878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
2070	15995	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	CHIR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4560	17698	30879	1.02	1.0E-20	BF115158.1	EST_HUMAN	211406.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
7034	20170	33592	0.74	1.0E-20	AF049567.1	EST_HUMAN	MER19 repetitive element;
9364	22439	35098	2.08	1.0E-20	11418497	NT	nr84606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1 L2 L1 repetitive element;
11847	24836	38530	2.03	1.0E-20	AF223391.1	NT	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
12461	25323		2.91	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							nc60g08.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1 L3 L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2979	16166		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AL003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-8J21
12174	25135		3.88	9.0E-21	AW898188.1	EST_HUMAN	RC3-NN0068-060503-021-503 NN0068 Homo sapiens cDNA
9011	22090		0.98	8.0E-21	AW674891.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11830	24819	38510	3.91	8.0E-21	AA809411.1	EST_HUMAN	CG5169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR
12345	25250		3.8	8.0E-21	O21330	SWISSPROT	cb7105.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1338835 3'
2130	15266	28385	3.85	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2130	15268	28386	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	16953	29958	1.36	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4389	17612		6.29	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6864	19728	33104	0.94	7.0E-21	AL163218.2	NT	2k67a06.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
8582	21663	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C018
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
10319	23354	36963	1.07	7.0E-21	AW856222.1	EST_HUMAN	Human chromosomal protein HMGC1 related gene
10934	24016	37648	1.94	7.0E-21	AA723404.1	EST_HUMAN	RCO-CT0301-271199-031-F03 CT0301 Homo sapiens cDNA
4220	17369	30358	0.75	6.0E-21	BE40861.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:398981 3' similar to
947	14120	27181	1.34	5.0E-21	5902031	NT	gb-M1438 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR18 OFR repetitive element
2354	15485	28517	1.23	5.0E-21	AA928194.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
4463	17623	30604	3.21	5.0E-21	BE98839.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
4809	14120	27181	1.18	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4923	18053	31039	8.33	5.0E-21	4885474	NT	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
6902	20217		0.77	5.0E-21	AW440864.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
7157	20291	33734	1	5.0E-21	BE859505.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
10801	23834	37457	0.54	5.0E-21	Q91690	SWISSPROT	783d11.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element
10801	23834	37458	0.54	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12259	25195		1.28	5.0E-21	AA393574.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
1772	14921	28015	1.86	4.0E-21	AA970713.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
							cg96a08.s1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:727878 5'
							cg96a08.s1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
							PMS3 MRNA; contains OFR.11 OFR repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	20147	33568	2.61	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTLM, complete cds
9983	23022	36614	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36842	0.51	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1884	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.st Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15479	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3149	16324	28936	6.41	3.0E-21	AJ007873.1	NT	Homo sapiens LOMD2B gene
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidease (dNT-2 gene), exons 1-5
5616	18810	31879	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidease (dNT-2 gene), exons 1-5
8856	19046		0.9	3.0E-21	AV681044.1	EST_HUMAN	AY681044 GLC Homo sapiens cDNA clone GLC0A10.3'
6308	19480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
7215	20080	33493	7.52	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9894	22834	36518	0.92	3.0E-21	AW697760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12879	26098	31665	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0468-170200-090-g12 HT0458 Homo sapiens cDNA
958	14131	27189	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27190	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
2703	15821	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15821	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18796	31846	1.66	2.0E-21	A1624582.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5604	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5694	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	z997a12.r1 Scores_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32678	0.74	2.0E-21	W44493.1	EST_HUMAN	z28b102.r1 Scores_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323667 5'
8467	21548	35078	0.58	2.0E-21	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
8568	21639	35178	8.13	2.0E-21	BE141765.1	EST_HUMAN	QV0-HT0103-091198-060-q11 HT0103 Homo sapiens cDNA
9023	22102	35642	3.27	2.0E-21	AU196779.1	EST_HUMAN	AU196779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11599	24652	38335	2.88	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element ;
							601880636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	2.0E-21	BE97828.1	EST_HUMAN	60168036F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	25389		6.44	2.0E-21	AF178815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1284	14440	27609	1.89	1.0E-21	AA567657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_Pv4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1434	14687		4.93	1.0E-21	AI601264.1	EST_HUMAN	ar88d12.x1 Barstead cdon HPLURB7 Homo sapiens cDNA clone IMAGE:2162343 3'
6816	19776		2.73	1.0E-21	AL079752.1	EST_HUMAN	DKFZp434i0830_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434i0830 5'
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	tg47a05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM PROTEIN (HUMAN);
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
13014	25667		1.67	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22 410-8
4530	17668	30654	2.38	9.0E-22	AI702438.1	EST_HUMAN	hs34a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:O15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
8803	21882	35420	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8803	21882	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37748	3.1	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSOCG05 5'
12007	24982	38696	1.39	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000384 5'
871	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	CMO-HT0178-281099-076-h05 HT0178 Homo sapiens cDNA
8080	21182		3.36	8.0E-22	AA046502.1	EST_HUMAN	z167a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
682	13667	26898	3.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4398	17541	30522	3.27	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5150	18272	31241	0.91	7.0E-22	AB008081.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8868	21967		1.24	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9032	22111	35653	2.77	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#38206) Homo sapiens cDNA clone HFBCF07
9802	22842	38419	2.05	7.0E-22	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
8438	21517		1.25	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2842812 3'
6846	19805	33192	3.27	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10525	23550	37167	2.98	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12833	25555		1.63	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCL_CGAP_Pv28 Homo sapiens cDNA clone IMAGE:3265898 3' similar to contains Alu repetitive element;
3726	16987		0.77	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8608	26224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10981	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	601682813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14154		1.34	3.0E-22	AI469679.1	EST_HUMAN	tm14h10.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L18593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element;
2636	15759	28873	1.33	3.0E-22	AI859038.1	EST_HUMAN	wl66b04.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
3763	16924		1.85	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.;
4922	18052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	Human chromosome 17 protein HMG1 related gene
8011	21081	34573	0.8	3.0E-22	P11369	SWISSPROT	gp28c07.x1 Soares_pregnant_Uterus_NHHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8425	21506		1.11	3.0E-22	BE156613.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
8430	21511	35042	1.88	3.0E-22	BE088841.1	EST_HUMAN	ENDONUCLEASE]
8553	21636	35172	1.14	3.0E-22	X60660.1	NT	QV0-HT0369-Q60200-099-112 HT0368 Homo sapiens cDNA
8555	21636	35173	1.14	3.0E-22	X60660.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	Rattus RY2G5 mRNA for a potential ligand-binding protein
2590	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	Rattus RY2G5 mRNA for a potential ligand-binding protein
3507	16674	28684	3.98	2.0E-22	8394043	NT	Y73d05.s1 Soares_melanocyte_ZNblm Homo sapiens cDNA clone IMAGE:267369 3'
4341	17484	30486	1.41	2.0E-22	AW817794.1	EST_HUMAN	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
5973	28614	32476	1.47	2.0E-22	W39456.1	EST_HUMAN	Homo sapiens protein Kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKG3), mRNA
6306	19476	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	PM1-ST0282-261199-001-412 ST0262 Homo sapiens cDNA
9904	22944	36529	1.78	2.0E-22	A1276522.1	EST_HUMAN	zz20f01.r1 Soares_senescent_fibroblasts_NHHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
10001	23039	36630	0.85	2.0E-22	AA718315.1	EST_HUMAN	RCO-TN0079-150900-025-H12 TN0079 Homo sapiens cDNA
10001	23039	36631	0.85	2.0E-22	AA718315.1	EST_HUMAN	d176h06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER29.13 MER29 repetitive element;
12056	25037	38745	1.52	2.0E-22	AW418660.1	EST_HUMAN	nv04h11.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
12139	26666	31954	2.33	2.0E-22	AL163280.2	NT	nv04h11.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
1927	15070	28175	2.05	1.0E-22	AW865517.1	EST_HUMAN	h224f04.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
2851	15744	28887	2.38	1.0E-22	U60871.1	NT	Homo sapiens chromosome 21 segment HS21C080
3487	16684	29676	1.53	1.0E-22	D14547.1	NT	PM4-SN0020-010400-009-n02 SN0020 Homo sapiens cDNA
7920	20971	34478	1.09	1.0E-22	BE084687.1	EST_HUMAN	Human DNA, SINE repetitive element
10776	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	Human familial Alzheimer's disease (S TM2) gene, complete cds
							MRO-BT0659-220200-002-n07 BT0659 Homo sapiens cDNA
							q209b07.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020961 3' similar to contains MER29.b2
							MER29 repetitive element;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23899	37433	1.05	1.0E-22	AB65435.1	EST_HUMAN	q209b07.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
13078	25707		12.31	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3661	16824	29833	0.74	8.0E-23	AF198349.1	NT	IL2-JM0078-070400-061-F11 UM0076 Homo sapiens cDNA
3385	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
11293	24359	38000	3.74	7.0E-23	5031952	NT	AY647246 GLO Homo sapiens cDNA clone GLCAWC07 3'
3520	16686		1.83	6.0E-23	AF198333.1	NT	Homo sapiens Ncl56 (D. melanogaster)-like protein (NOT56L) mRNA
4383	17528	30507	1.15	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12288	25211	32097	4.93	6.0E-23	AF224669.1	NT	Homo sapiens chromosome 21 segment HS21C049
12283	25211	32098	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12483	25335	32058	3.18	6.0E-23	AI209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5560	18757	31798	4.01	5.0E-23	UB2871.2	NT	q35b03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
6369	26824	32898	3.69	5.0E-23	AF179818.1	NT	SW.MY.10_MOUSE P23249 PROTEIN MOV-10.1
7695	26824	32898	2.78	5.0E-23	AF179818.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
6570	18732	33110	0.67	3.0E-23	AL163227.2	NT	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathepsin
6670	19732	33111	0.67	3.0E-23	AL163227.2	NT	(CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
8022	21105	34622	3.26	3.0E-23	AA130165.1	EST_HUMAN	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
8450	22566	36130	3.72	3.0E-23	Z70664.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
9450	22566	36131	3.72	3.0E-23	Z70664.1	NT	Homo sapiens chromosome 21 segment HS21C027
10523	23558		1.42	3.0E-23	AW897627.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
11372	24433		1.35	3.0E-23	AF280107.1	NT	235509.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to
683	13868	26899	3.69	2.0E-23	AJ289880.1	NT	contains MER29.12 MER29 repetitive element;
1166	15898		3.46	2.0E-23	M56270.1	NT	Human endogenous retroviral element HC2
2856	15970	28078	1	2.0E-23	P22105	SWISSPROT	Human endogenous retroviral element HC2
2856	15970	28080	1	2.0E-23	P22105	SWISSPROT	Human endogenous retroviral element HC2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3457	16324		1.11	2.0E-23	AI201458.1	EST_HUMAN	qs73f11.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3810	16970		3.53	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4085	17240	30246	4.43	2.0E-23	H59931.1	EST_HUMAN	MF3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA
4085	17240	30247	4.43	2.0E-23	H59931.1	EST_HUMAN	yt16a02.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:205418 5'
							yt16a02.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8057	21140		6.28	2.0E-23	AF280107.1	NT	Human sapiens chromosome 21 segment HS21C103
9044	22123	36865	0.95	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12265	25199		6.7	2.0E-23	MS2658.1	NT	Human sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12844	25531		3.68	2.0E-23	AF009680.1	NT	Human sapiens OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
12883	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	AUT33631 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4650	17786	30769	1.57	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4888	18018		5.42	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5851	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
							zw82c08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782898 5' similar to contains PTR5.L2
							PTR5 repetitive element ;
8551	21632	35168	4.61	1.0E-23	AA448097.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37825	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37628	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301782F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
13082	26074	31654	1.35	1.0E-23	AW901816.1	EST_HUMAN	QV0-NN1020-170400-195-at11 NN1020 Homo sapiens cDNA
							ab75a08.s1 Strazene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
							TR:E19822 E19822 CA PROTEIN. ;
566	13759		1.67	9.0E-24	AA663213.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4771	17906	30888	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4771	17906	30889	1.12	8.0E-24	P23269	SWISSPROT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
6578	19740	33121	0.95	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.94	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-306 DT0047 Homo sapiens cDNA
5281	18400		16.79	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1_1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A2311 5'
							repetitive element contains MER19.12 MER19 repetitive element ;
10376	23981		1.61	7.0E-24	AW303317.1	EST_HUMAN	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
724	13006		2.21	6.0E-24	AB001421.1	NT	Homo sapiens chromosome 21 segment HS21C049
861	14038	27100	12.8	6.0E-24	AL163248.2	NT	Homo sapiens chromosome 21q22, segment 3/3
4078	17234	30241	9.39	5.0E-24	AJ228043.1	NT	Homo sapiens 959 kb contig between AVL1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7935	20885	34493	1.27	5.0E-24	AF223391.1	NT	

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17614		0.9	4.0E-24	BF369469.1	EST_HUMAN	RC0-GN0090-250900-022-h09 GN0090 Homo sapiens cDNA
6052	19234	32559	2.77	4.0E-24	AA594178.1	EST_HUMAN	nm31h06.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVVK
8880	21959	35494	0.71	4.0E-24	AW813711.1	EST_HUMAN	P31765 POL POLYPROTEIN :
11454	24514	38182	2.05	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-096 ST0197 Homo sapiens cDNA
12669	25448	32054	4.02	4.0E-24	AB028016.1	NT	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
							Homo sapiens mRNA for KIAA1093 protein, partial cds
7228	20134	33551	0.73	3.0E-24	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
7229	20134	33552	0.73	3.0E-24	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.> hh88c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867850 3' similar to contains MER28.b2 MER29 repetitive element :
8618	21638		2.94	3.0E-24	AW614871.1	EST_HUMAN	EST374149 IMAGE resequencer, MAGG Homo sapiens cDNA
8873	21753		1.24	3.0E-24	AW682078.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
9695	22627	36198	3.79	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12756	25501	32034	1.34	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053398 5'
2422	15951	28678	2.55	2.0E-24	AA101539.1	EST_HUMAN	zp11109.r1 Stragelene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3899	17058		0.82	2.0E-24	AW888189.1	EST_HUMAN	RC3-NN0068-080500-021-503 NN0068 Homo sapiens cDNA
7515	28219		0.63	2.0E-24	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
7643	20712	34191	0.9	2.0E-24	AF086924.1	NT	Mus musculus thymocyte-interacting citron kinase (Chik) mRNA, complete cds
7648	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-6H13
8938	22017	35559	3.81	2.0E-24	AL119158.1	EST_HUMAN	DKFZp791L1712_r1 781 (synonym: ham2) Homo sapiens cDNA clone DKFZp791L1712 5'
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	Y82809.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element :
10058	23098	36698	1.08	2.0E-24	A1521759.1	EST_HUMAN	h77a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
10058	23098	36699	1.06	2.0E-24	A1521759.1	EST_HUMAN	h77a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12580	26153	27872	21.43	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1731	14881		4.81	1.0E-24	AW820194.1	NT	Homo sapiens GSH-127 protein (LOC51646), mRNA
2738	15855		1.65	1.0E-24	AW820194.1	EST_HUMAN	QY0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3085	16201	29278	0.72	1.0E-24	D88423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4385	17628		1.93	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	19895	33068	1.13	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C29 (K11-c29), mRNA
7720	20784	34272	4.85	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20959	34485	5.07	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0166-271186-005-409 HT0166 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901164.1	EST_HUMAN	CMO-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
11999	24984	38689	1.37	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5111	18239	31205	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne92a10.s1 NCL CGAP_K1d1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8413	21494	35025	3.7	7.0E-25	AA488646.1	EST_HUMAN	ne09a09.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
12003	24988	38693	3.64	7.0E-25	AA583540.1	EST_HUMAN	ne25h06.s1 NCL CGAP_P71 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
7131	18597		5.04	6.0E-25	W87623.1	EST_HUMAN	P36103 PROBABLE 90S RIBOSOMAL PROTEIN L14EA. ;
7899	20861	34458	11.72	6.0E-25	7305360	NT	zh65h07.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
1683	14835	27920	1.61	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
11896	24649	38333	3.12	5.0E-25	AW979107.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
1478	14631	27716	2.66	4.0E-25	T98107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
3489	16566		2.81	4.0E-25	AW887671.1	EST_HUMAN	ye56h04.r1 Soares_fetal_liver_spleen_INFLS_Homo sapiens cDNA
4436	17576		4.06	4.0E-25	BE170957.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
10144	23182	36779	0.83	4.0E-25	AA388873.1	EST_HUMAN	QV3-HT0543-140400-149-s11 HT0543 Homo sapiens cDNA
2256	15389	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	EST197317 Thymus Homo sapiens cDNA 5' end similar to EST containing O family repeat
3396	16566	29581	3.12	3.0E-25	8923321	NT	RC5-BT0377-131299-031-F02 BT0377 Homo sapiens cDNA
3396	16566	29582	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	P28622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
8632	21613	35149	5.42	3.0E-25	AL163210.2	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
11287	24353	37953	2.7	3.0E-25	AA578013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1378	14593	27807	4.9	2.0E-25	5032158	NT	ne30h10.s1 NCL CGAP_P71 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.11 L1
2382	15513	28641	7.33	2.0E-25	BE888016.1	EST_HUMAN	repetitive element ;
2893	15731	28848	3.71	2.0E-25	P17008	SWISSPROT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	601611530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9967	17460	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9967	23006	36601	2.13	2.0E-25	AL449573	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
375	13583	26617	0.81	1.0E-25	AL040229.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
1277	14434		2.07	1.0E-25	9635487	NT	DKFZp434h0313_r1 434 (synonym: h3e3) Homo sapiens cDNA clone DKFZp434h0313 5'
							Human endogenous retrovirus, complete genome

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-k09 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19855		0.95	1.0E-25	AA189080.1	EST_HUMAN	zq4506.s1 Stratiene N1T neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Ali repetitive element;
6830	25938	33686	2.95	1.0E-25	AA582860.1	EST_HUMAN	nt54h1.s1 NC1_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:108749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	z186g04.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains
9748	22810	36388	1.32	1.0E-25	X60660.1	NT	Ptr5.13 PTR5 repetitive element;
9748	22810	36389	1.32	1.0E-25	X60660.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37920	3.11	1.0E-25	U93163.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
12280	25209	38364	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38365	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2663	16678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11262	24321		2.35	9.0E-26	AL905368.1	EST_HUMAN	QV-BT087-301298-006 BT087 Homo sapiens cDNA
12140	25901		5.33	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5811	18001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H1.sapiens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340183.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11988	24651		6.85	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratiene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:648943 6' similar to db:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	25996		5.49	7.0E-26	AW854559.1	EST_HUMAN	EST366629 IMAGE resequences, MAGC Homo sapiens cDNA
2300	15432	28565	3.83	6.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3427	16596	29611	0.69	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stratiene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 6'
10753	23786	37400	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10753	23788	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11879	24954	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14366	27426	0.89	5.0E-26	AI708235.1	EST_HUMAN	ss38h08.x1 Barstead acta1 HPLRB6 Homo sapiens cDNA clone IMAGE:2318519 3' similar to WP:F49C12.11 CE03371;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	A1708235.1	EST_HUMAN	as38f08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to
9612	22667		3.29	4.0E-26	7657670	NT	WPF49C12.11 CE03371 ;
10867	23981	37613	2.84	4.0E-26	BE266187.1	EST_HUMAN	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
11804	24667	38342	1.38	4.0E-26	AL163246.2	NT	001191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3835210 5'
1797	14946	28038	1.25	3.0E-26	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C046
2059	15200	28314	1.14	3.0E-26	ALD46865.2	EST_HUMAN	Human DNA, SINE repetitive element
2088	15228		3.34	3.0E-26	AA115885.1	EST_HUMAN	DKFZp434066_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434066 5'
3678	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zn30d08.r1 Striatene neuroepithelium NT2RAMI 837234 Homo sapiens cDNA clone IMAGE:548943 5'
3678	17037	30036	1.41	3.0E-26	AA152464.1	EST_HUMAN	similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
7051	20104	33521	6.09	3.0E-26	BF245448.1	EST_HUMAN	z030f10.r1 Striatene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11867	24855	38550	1.97	3.0E-26	AW875651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11867	24855	38551	1.97	3.0E-26	AW875651.1	EST_HUMAN	z030f10.r1 Striatene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11902	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
899	13982	26915	6.84	2.0E-26	AL163282.2	NT	001864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
1917	18060		3.07	2.0E-26	AL038089.2	EST_HUMAN	QV2-PT0012-040400-124-s05 PT0012 Homo sapiens cDNA
3303	16477	29499	5.22	2.0E-26	X86694.1	NT	QV2-PT0012-040400-124-s05 PT0012 Homo sapiens cDNA
10991	24070		1.93	2.0E-26	D87675.1	NT	m37d05.s1 NCI_OGAP_GC8 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
11493	24551	38228	2.96	2.0E-26	AB01412.1	EST_HUMAN	OFR repetitive element ;
11704	24701		2.06	2.0E-26	AF05066.1	NT	Homo sapiens chromosome 21 segment HS21C082
12989	28275		1.78	2.0E-26	AB037856.1	NT	DKFZp566L171_s1 588 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
12904	28098	31658	2.33	2.0E-26	11435947	NT	Musculus mRNA for astrocytic phosphoprotein, PEA-15
139	13365	28398	8.96	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
2105	15244	28365	1.42	1.0E-26	AL038363.2	EST_HUMAN	lo86a01.x1 NCI_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu
2751	15668		6.28	1.0E-26	AF261085.1	NT	repetitive element-contains element MER20 MER20 repetitive element ;
6980	20208		2.89	1.0E-26	BE165980.1	EST_HUMAN	Homo sapiens MHC class 1 region
11131	24203		1.96	1.0E-26	AL038487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
12855	26178		2.77	1.0E-26	H55093.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	QV4-HT0598-020300-123-s02 HT0598 Homo sapiens cDNA
							DKFZp434H1910_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
							MR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
							DKFZp566C2148_r1 588 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2148 5'
							CHR220322 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							U1HF-BMO-adw-d-10-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9503	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12143	25118		6.5	9.0E-27	BF445556.1	EST_HUMAN	na03c07.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3233644 3' similar to contains OFR.t1 OFR repetitive element ;
11	13249	28249	4.22	8.0E-27	AI831492.1	EST_HUMAN	wf49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14801	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
1448	14801	27679	23.84	8.0E-27	AW162737.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	15369	28499	1.82	8.0E-27	AW864775.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558
3254	16428	29446	1.8	8.0E-27	P12236	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN);
3434	16602	29621	0.75	8.0E-27	AF181897.1	NT	PM2-SN0018-220300-002-e07 SN0018 Homo sapiens cDNA
5912	18002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
7117	18643		2.65	8.0E-27	BE928660.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7192	20057	33487	2.49	8.0E-27	N84970.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB08 5'
9410	22484	36048	1.63	8.0E-27	AW857570.1	EST_HUMAN	MR4-BT0399-250800-204-d08 BT0399 Homo sapiens cDNA
9410	22484	36049	1.53	8.0E-27	AW857579.1	EST_HUMAN	J1761F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1761 5' similar to
701	13894		1.77	7.0E-27	Z70684.1	NT	REPETITIVE ELEMENT L1
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element HC2
8058	22137		0.97	7.0E-27	D66984.1	NT	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
10988	24067		3.7	7.0E-27	AL1271735.1	NT	O76040 ORF2: FUNCTION UNKNOWN ;
10984	24046	37878	3.21	6.0E-27	M26697.1	NT	Human mRNA for KIAA0231 gene, partial cds
12094	25074	38781	1.55	6.0E-27	U93163.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
7854	21004		0.73	6.0E-27	AL163303.2	NT	Human nucleolar protein (B23) mRNA, complete cds
10442	23477	37081	3.21	6.0E-27	BF666614.1	EST_HUMAN	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10442	23477	37082	3.21	6.0E-27	BF666614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
6883	20035	33444	1.65	4.0E-27		NT	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
					9910569	NT	602121491F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Slap), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	21207		0.98	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9945	22984	36577	0.61	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-182-b10 OT0033 Homo sapiens cDNA
11903	24691	36592	2.62	4.0E-27	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2099	15239	28361	7.1	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4388	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-060100-001-d11 BT0527 Homo sapiens cDNA
5462	19862	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	501458531F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3662086 5'
42	13280	26286	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1044	15087		24.24	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.st NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
3178	16353		13.94	2.0E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976879 3' similar to TR:078040
3295	16470	29489	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19967	33373	0.79	2.0E-27	H02855.1	EST_HUMAN	X36601.r1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:150840 5' similar to
8282	21394	34883	1.17	2.0E-27	A1866347.1	EST_HUMAN	SP:HMGC_MOUSE_Q02591 HOMEBOX PROTEIN ;
9469	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	w128g07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426266 3'
9995	23033	36825	0.83	2.0E-27	X60658.1	NT	nk08h05.st NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
10241	23276	36868	1.45	2.0E-27	M78590.1	EST_HUMAN	repetitive element ;
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
11197	24266	37801	3.61	2.0E-27	AU121685.1	EST_HUMAN	ES-T00738 Fetal brain; Striatogene (ca54936206) Homo sapiens cDNA clone HFBCF07
11777	15087		6.43	2.0E-27	AA565345.1	EST_HUMAN	EST00738 Fetal brain; Striatogene (ca54936206) Homo sapiens cDNA clone HFBCF07
12107	25087	38761	1.64	2.0E-27	AF216650.1	NT	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
449	13645		2.34	1.0E-27	AL163246.2	NT	nk01b10.st NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000689 similar to gb:M17886 60S
1021	14192	27251	4.97	1.0E-27	AB026998.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
8674	19833	33222	0.51	1.0E-27	6005855	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33568	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
7010	20146	33567	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000095C10
8803	21888	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9186	22284		1.69	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
9823	22663	36551	2.65	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24690	38694	3.05	1.0E-27	AF11093.1	NT	Bos taurus latrophilin 3 splice variant b5ah mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	28567	2.17	9.0E-28	AU126280.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313 ;
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	AU126280 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
12224	25173		3.04	9.0E-28	BF377659.1	EST_HUMAN	z018g12.s1 Sitratogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
12565	26003		13.39	8.0E-28	AW167571.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
11483	24522	38192	1.65	7.0E-28	11417866	NT	TR:O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ;
12181	25141		5.04	7.0E-28	AV735348.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
9119	22188		1.28	6.0E-28	AF016052.1	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAXA12 5'
328	13542		2.75	5.0E-28	AB21003.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
4116	17270	30269	35.94	5.0E-28	R70762.1	EST_HUMAN	aa60e03.1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
2869	15809	28926	1.46	4.0E-28	AW195005.1	EST_HUMAN	repetitive element; contains element P/TRS repetitive element ;
3177	16352	28358	1.34	4.0E-28	BE409100.1	EST_HUMAN	wo18c07.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:24555692 3' similar to contains THR.b1
7483	20558	34030	3.56	4.0E-28	AI198941.1	EST_HUMAN	THR repetitive element ;
11105	24177		4.19	4.0E-28	AF029308.1	NT	y69f10.11 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:145443 5'
11255	24324		14.69	4.0E-28	AB038241.1	NT	xn33c09.x1 NCI CGAP K1411 Homo sapiens cDNA clone IMAGE:2685504 3' similar to SW:G095_HUMAN
11278	20558	34030	4.34	4.0E-28	AI198941.1	EST_HUMAN	q06f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:3635305 5'
12622	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
12773	26058		1.62	4.0E-28	AW862350.1	EST_HUMAN	q06f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
							RC3-CT0254-240400-210-f12 CT0254 Homo sapiens cDNA
							RC3-CT0379-070100-031-h01 CT0379 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1312	14468		2.29	3.0E-28	AF165382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF009660.1	NT	Homo sapiens I cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9027	22106	35647	2.28	3.0E-28	BF354030.1	EST_HUMAN	NR3-HT0713-280500-013-009 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U53688.1	NT	Homo sapiens MHC class 1 region
12653	25433		3.77	3.0E-28	AI831991.1	EST_HUMAN	wj98f07.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
12803	25536		3.29	3.0E-28	BE092801.1	EST_HUMAN	RC2-BT0642-210200-013-003 BT0642 Homo sapiens cDNA
12865	25576	31983	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12865	25576	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
91	13326	26354	12.79	2.0E-28	BE082187.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens TIGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI548634.1	EST_HUMAN	qs3b06.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1810483 3' similar to contains L1.b2 L1 repetitive element;
3446	16614	26632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	19604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	h76c03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
6460	19627		3	2.0E-28	BF212905.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.93	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
11913	24500	39603	2.52	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424		1.74	2.0E-28	H06376.1	EST_HUMAN	y78c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1508	14661	27744	2.55	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2294	15426	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
4891	17826		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8044	21127		1.95	1.0E-28	11428985	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA
8208	21260		3.03	1.0E-28	8022763	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36099	4.75	1.0E-28	AA308744.1	EST_HUMAN	EST178615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral L TR
10080	23118	36720	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12188	25145		7.86	1.0E-28	AA054182.1	EST_HUMAN	z51c01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380448 5'
13013	25881		4.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	26122	31643	1.8	9.0E-29	AW663987.1	EST_HUMAN	h176g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOPHOSPHATASE 50 PROTEIN
1632	14784	27870	1.98	7.0E-29	AW868447.1	EST_HUMAN	EST378621 IMAGE resequenced, MAGI Homo sapiens cDNA
13197	25779		9.03	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	6.0E-29	AI939749.1	EST_HUMAN	w68950.1x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O15475
12495	25342		5.19	6.0E-29	BE940436.1	EST_HUMAN	O16475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
12887	25395		2.1	6.0E-29	BF568067.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-29	AL183203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
8029	22008		8.35	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21 C003
12785	25531		1.49	5.0E-29	BE612449.1	EST_HUMAN	RC3-OT0081-170300-011-c12 OT0091 Homo sapiens cDNA
3304	16478		2.28	4.0E-29	AI752367.1	EST_HUMAN	601451827F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3855728 5'
8133	18312		7.08	4.0E-29	BE164630.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cello Homo sapiens cDNA clone NHTBC_cn15c02 random
8272	21354	34870	0.64	4.0E-29	AI678101.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8272	21354	34871	0.64	4.0E-29	AI678101.1	EST_HUMAN	w635g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8944	22023	35563	3.59	4.0E-29	JO4988.1	NT	MER29.12 MER29 repetitive element;
4838	17874	30668	1.31	3.0E-29	AB042287.1	NT	Human 60 kD heat shock protein gene, complete cds
4855	17988	30976	1.1	3.0E-29	BF333238.1	EST_HUMAN	Homo sapiens PTS gene for 6-pyruvyltetrahydropterin synthase, complete cds
5053	19235	32560	0.83	3.0E-29	BE314018.1	EST_HUMAN	QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	601152657F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3508627 5'
9500	22556	38119	1.22	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
9731	22796		1.49	3.0E-29	AL163246.2	NT	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
10164	23201		0.61	3.0E-29	BE350127.1	EST_HUMAN	repetitive element contains MER19.12 MER19 repetitive element;
11546	24602	38278	2.26	3.0E-29	AA403053.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21 C046
12386	25272		1.38	3.0E-29	D63882.1	NT	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
13092	26132		1.62	3.0E-29	D63882.1	NT	MER29 repetitive element;
503	13608	26727	0.98	2.0E-29	AF084869.1	NT	z62b01.11 Soares_Testis NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
505	13699	26728	0.98	2.0E-29	AF084869.1	NT	G1335769 GAG-POL POLYPROTEIN;
							Human HsLIM15 mRNA for HsLIM15, complete cds
							Human HsLIM15 mRNA for HsLIM15, complete cds
							Homo sapiens envelope protein RIC-5 (env) gene, complete cds
							Homo sapiens envelope protein RIC-6 (env) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1593	14716	27794	7.8	2.0E-29	AI963604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1593	14716	27795	7.8	2.0E-29	AI963604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5946	19132	32446	0.78	2.0E-29	AI082459.1	EST_HUMAN	os71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1:12 L1 repetitive element ;
6309	19481	32835	1.49	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355860 3' similar to contains element MER6 repetitive element ;
7732	19481	32835	1.28	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355860 3' similar to contains element MER6 repetitive element ;
8164	21246	34766	1.16	2.0E-29	BE867157.1	EST_HUMAN	601442206F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3846648 5'
8777	21856	35399	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC55242), mRNA
8777	21856	35399	0.61	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC55242), mRNA
9708	22767	36327	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22767	36328	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11787	24760		1.67	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnal (SPF31), mRNA
8992	22071	35611	8.27	1.0E-29	AW983890.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10850	23883	37503	2.81	1.0E-29	X60658.1	NT	Rattus RYA3 mRNA for a potential ligand-binding protein
6712	19870	33261	3.53	9.0E-30	AA781215.1	EST_HUMAN	hz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1286332 3' similar to contains MER4.b1 MER4 repetitive element ;
12266	25200		4.55	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
6449	19616		10.5	8.0E-30	F09688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8465	21546	35076	2.26	8.0E-30	AA333973.1	EST_HUMAN	EST197317 Thymus I Homo sapiens cDNA 5' and similar to EST containing O family repeat
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	P72.1_13_B11.r tumor2 Homo sapiens cDNA 3'
1546	14697		1.07	7.0E-30	BE001133.1	EST_HUMAN	PIV4-BT0724-150400-004-311 BT0724 Homo sapiens cDNA
1814	14963	28056	1.57	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3259	19433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	QV6-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
4881	19433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	QV6-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF17727.1	NT	Homo sapiens CTCL tumor antigen se20-10 mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17275	30274	43.22	5.0E-30	AI399992.1	EST_HUMAN	ig2403.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element.
5353	25928		5.79	5.0E-30	U87931.1	NT	Human acetylcholinesterase (AChE) gene, exon 7
11126	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	15344	28470	2.38	4.0E-30	AW693747.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2210	15344	28471	2.38	4.0E-30	AW693747.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
9109	22185	35729	1.55	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	AI336551.1	EST_HUMAN	qq93c05.x1 Soares_tetrahymena_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
3853	17013	30013	1.15	3.0E-30	AF128853.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8138	21220		0.63	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8653	21763		0.45	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10649	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3 MER29 repetitive element;
11462	24541	38211	1.52	3.0E-30	P34059	SWISSPROT	TRANSCRIPTION FACTOR AP-2
692	13876	26908	1.42	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-168-h03 CT0307 Homo sapiens cDNA
1106	14273		2.53	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1509	14652	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	RG5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2779	15895	29005	9.93	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
2886	16162	29179	6.83	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3886	17048	30048	1.95	2.0E-30	AW206581.1	EST_HUMAN	U1H-B11-af0-c-12-Q.U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722568 3'
4900	18030	31018	2.02	2.0E-30	BE268945.1	EST_HUMAN	601119860FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4900	18030	31019	2.02	2.0E-30	BE268945.1	EST_HUMAN	601119860FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
8734	21814	35349	4.69	2.0E-30	CT6839.1	EST_HUMAN	CT6839 Human placenta cDNA (T Fujitara) Homo sapiens cDNA clone GEN-570C01 5'
8836	21916	35452	1.71	2.0E-30	BE870617.1	EST_HUMAN	7e37c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8836	21915	35453	1.71	2.0E-30	BE870617.1	EST_HUMAN	7e37c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10201	23238	35628	3.78	2.0E-30	AW971568.1	EST_HUMAN	ES1383557 IMAGE resequences, MAGL Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	23322	36924	6.31	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
297	13514	28548	10.87	1.0E-30	C18939.1	EST_HUMAN	THR repetitive element;
							C18939 Human placenta cDNA (T Fujiwara) Homo sapiens cDNA clone GEN:570C01 5'
561	13744	28769	1.62	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains
734	13916	26956	5.15	1.0E-30	AL163203.2	NT	MER1.13 MER1 MER1 repetitive element;
2286	15418	28550	11.56	1.0E-30	AA664377.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
2533	16658	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	ac77b08.s1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:968599 3'
3120	16286	29310	0.91	1.0E-30	AA315045.1	EST_HUMAN	602022560F1 NCL_CGAP_Brn57 Homo sapiens cDNA clone IMAGE:4157991 5'
7901	20953	34490	1.56	1.0E-30	BF183230.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
8176	21258	34780	0.49	1.0E-30	BE061888.1	EST_HUMAN	601809632F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
12786	26117		1.57	1.0E-30	AA29921.1	EST_HUMAN	MRO-BT0249-091299-101-g01 BT0249 Homo sapiens cDNA
12937	26025		5.31	1.0E-30	H55583.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
3862	17022	30020	0.8	9.0E-31	T73025.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3862	17022	30021	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stralagene liver (#637224) Homo sapiens cDNA clone IMAGE:85370 5'
						EST_HUMAN	yc65e08.r1 Stralagene liver (#637224) Homo sapiens cDNA clone IMAGE:85570 5'
8619	21600	35135	0.98	9.0E-31	R18214.1	EST_HUMAN	yc69b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8519	21600	35136	0.98	9.0E-31	R18214.1	EST_HUMAN	y69b08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8825	21604		1.99	9.0E-31	Z39293.1	EST_HUMAN	RELATED PROTEIN RAB-2 (HUMAN);
8827	21606	35445	0.55	9.0E-31	AF078779.1	NT	HS035F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
13183	25776	31934	1.29	9.0E-31	6756441	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1102	14267	27325	2.52	8.0E-31	8923389	NT	Mus musculus syndecan 4 (Scd4), mRNA
2484	15611		7.93	8.0E-31	AL163208.2	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
729	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
2733	15850	28962	2.1	7.0E-31	BE326517.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2733	15850	28963	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8595	21676	35212	1.02	7.0E-31	AF208641.1	NT	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8595	21676	35213	1.02	7.0E-31	AF208641.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8595	21676	35213	1.02	7.0E-31	AF208641.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8468	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3769	16930		3.42	6.0E-31	AF223391.1	NT	
8347	21428		1.39	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8526	21607	35146	0.75	6.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
10976	24055	37689	1.43	6.0E-31	AL119105.1	EST_HUMAN	AL119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12327	25236	32108	3.7	6.0E-31	AW372898.1	EST_HUMAN	RG5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
12459	25947		2.54	6.0E-31	BE894488.1	EST_HUMAN	601433087f1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	28450	3.39	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	13420	28451	3.39	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8840	21720		1.29	5.0E-31	BF088540.1	EST_HUMAN	7k06f04.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13637 Q13537 SIMILAR TO POGO ELEMENT, contains L1.1 L1 repetitive element;
609	13768		3.02	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
1861	15007		2.09	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2849	15933		1.57	4.0E-31	5730038	NT	Homo sapiens SET domain and manner transposase fusion gene (SETMAR) mRNA
10764	23767	37402	0.46	4.0E-31	AF084464.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
12787	23528		1.55	4.0E-31	11430273	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
12924	25609		2	4.0E-31	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2860	15782	28697	1.75	3.0E-31	6005871	NT	Homo sapiens SEC83, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
7494	20599	34041	8.04	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUF8) mRNA
7663	20790	34208	1.23	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8355	21436		1.51	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
9779	22819	36397	2.59	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10822	23855	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	2i06d04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10867	23952	37562	2.03	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (R1G PROTEIN)
11421	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	60145853f1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862085 5'
1807	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	QV2-L-T0051-260300-111-033 L-T0051 Homo sapiens cDNA
2288	15420	28552	1.05	2.0E-31	A1393385.1	EST_HUMAN	tg44g06.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2111872 3'
2418	15545	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	DKFZ761G1513_1 761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:2111872 3'
2511	15637	28758	4.63	2.0E-31	AA459824.1	EST_HUMAN	ae88f11.s1 Stralagene fetal retina 897202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element:
5389	18591	31563	0.78	2.0E-31	AW444468.1	EST_HUMAN	UI-H-B13-akb-f09-0-UI s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'

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5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9277	22363		1.53	2.0E-31	AA87764.1	EST_HUMAN	m06004.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPARENT ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9408	22482	38046	3.46	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUALB07 5'
10110	23148	36749	1.1	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUALB07 5'
10280	23315	36814	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3388310 5'
10280	23315	36815	2.75	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3388310 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12578	26202		2.59	2.0E-31	AI114827.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
17	13255	26258	9.91	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1698	14848	27932	2.56	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1698	14848	27933	2.66	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1698	14848	27934	2.56	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
5407	18609	31581	3.97	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-408_1 ST0220 Homo sapiens cDNA
6261	19435	32781	2.57	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
7441	20518	33090	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8005	21055	34567	1.35	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10441	23476	37080	0.5	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11156	24227	37857	2.35	1.0E-31	AI086434.1	EST_HUMAN	q21103.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN. ;
6776	19931	33327	2.19	9.0E-32	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAAG01 5'
7530	20803	34077	0.66	9.0E-32	L31170.1	NT	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7766	20825		0.91	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2139	15275	28397	5.1	8.0E-32	AI056770.1	EST_HUMAN	zr15a09.x1 Scorec fetal liver spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5599	18794	31843	0.77	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA Human chromosome 22 Immunoglobulin V(K) gene, part with 5' breakpoint between orthon and neighbouring non-amplified region
12408	25285		2.36	7.0E-32	X17283.1	NT	
7523	20596		1.32	6.0E-32	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12869	26181		2.5	6.0E-32	AA864653.1	EST_HUMAN	oh37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1456972 3' similar to contains L1; L3 L1 repetitive element:
1059	14225	27282	10.42	6.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
954	14127		1.64	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7779	20835	34326	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-H05 BT0311 Homo sapiens cDNA
468	13693	26899	2.84	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731600.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAKC07 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (rithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.76	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (rithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9594	22649	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9594	22649	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
11166	24237	37858	3.43	3.0E-32	AA77621.1	EST_HUMAN	265a07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR18 THR repetitive element:
12433	25307		7.95	3.0E-32	BE278086.1	EST_HUMAN	601156285FT NIH_JMGC 21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (rithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (rithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
13020	25671		6.47	3.0E-32	BE278086.1	EST_HUMAN	601156285FT NIH_JMGC 21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32907	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6608	19786	33166	5.56	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6608	19786	33167	5.56	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8473	21594	35085	3.34	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21594	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16338		1.26	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_JMGC 9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20065	33478	6.64	1.0E-32	11439783	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8785	21874	35413	4.56	1.0E-32	AA720574.1	EST_HUMAN	nv21g02.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241198 3' similar to contains THR.13 THR repetitive element:

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3670	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07cd5.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539
6550	16712		3.17	9.0E-33	AF223391.1	NT	WW DOMAIN BINDING PROTEIN 11.;
8888	22067	35607	1.81	9.0E-33	BF347228.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11038	24117		4.55	9.0E-33	AL163280.2	NT	602021164F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI590116.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2714	15832		7.85	7.0E-33	AV730056.1	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
3314	16487		15	7.0E-33	AW971307.1	EST_HUMAN	6012009.x1 NCL CGAP_Lu2 Homo sapiens cDNA clone IMAGE:2178909 3' similar to contains OFR.11 OFR
9147	22228		0.87	7.0E-33	X54890.1	NT	repetitive element:
11067	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
11526	24592	38258	1.59	7.0E-33	AW971698.1	EST_HUMAN	EST383396 IMAGE resequences, MAGL Homo sapiens cDNA
12413	25292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
3830	16990		0.93	6.0E-33	AL163285.2	NT	602021164F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6192	19368	32717	0.91	6.0E-33	F30631.1	EST_HUMAN	EST383357 IMAGE resequences, MAGL Homo sapiens cDNA
6192	16368	32718	0.91	6.0E-33	F30631.1	EST_HUMAN	not16h01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1
8778	21657	35400	1.86	6.0E-33	J04038.1	NT	repetitive element:
8899	21978	35517	3.12	6.0E-33	11429168	NT	Homo sapiens chromosome 21 segment HS21C085
10214	23250	36839	2.03	6.0E-33	6755609	NT	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
10214	23250	36840	2.03	6.0E-33	6755609	NT	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
1818	14697		1.9	5.0E-33	BF373515.1	EST_HUMAN	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
1831	15074		1.32	5.0E-33	11141884	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
1947	15090	28190	1.63	5.0E-33	4507208	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1947	15090	28191	1.63	5.0E-33	4507208	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
2346	15477	30312	2.92	5.0E-33	AL153285.2	NT	QY1-FT0168-100700-271-a02 FT0168 Homo sapiens cDNA
4169	17319	37057	0.98	5.0E-33	AB014599.1	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
10454	23489	37057	0.92	5.0E-33	AW264679.1	EST_HUMAN	Homo sapiens spermidine synthase (SRM) mRNA
10454	23489	37058	0.92	5.0E-33	AW264679.1	EST_HUMAN	Homo sapiens spermidine synthase (SRM) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	25185		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1152	14316		2.25	4.0E-33	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2194	15329	28454	3.37	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15518		1.16	4.0E-33	AAG26621.1	EST_HUMAN	ab51b11.t1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2610	15734	28850	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4806	17743	30722	2.38	4.0E-33	AW293349.1	EST_HUMAN	U1H-B12-ah-c-03-Q.U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA053053.1	EST_HUMAN	z71a08.t1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:610038 5' similar to gb:X12671.mn1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	18687	33060	0.78	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	18687	33061	0.78	4.0E-33	8393984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.62	3.0E-33	BE360127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER29 repetitive element;
1114	14278		5.83	3.0E-33	BE360127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER29 repetitive element;
2522	16084		1.16	3.0E-33	AV647851	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLOBCE09 3'
10555	23689	37298	0.87	3.0E-33	AA681510.1	EST_HUMAN	ak32b12.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE.;
18	13256		1.67	2.0E-33	A1160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
107	13256		5.53	2.0E-33	A1160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
4539	17577		4.53	2.0E-33	BE156039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
5100	18228	31199	8.64	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.t1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844358 5' similar to gb:X00734.cde1 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31294	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-42 (SIRP-42), mRNA
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-42 (SIRP-42), mRNA
6553	19715	33091	1.39	2.0E-33	A1277492.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-42 (SIRP-42), mRNA
9301	22377		2.15	2.0E-33	A1052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9	13247		1.61	1.0E-33	AF003628.1	NT	gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
7565	20537	34113	0.86	1.0E-33	MT13975.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							Homo sapiens protein kinase C beta-II type (PRKCBT1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10227	28229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11802	24655	38340	1.56	1.0E-33	AW98818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11982	24947	38682	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW60491.1	EST_HUMAN	RCS-NN1055-280400-021-G03 NN1055 Homo sapiens cDNA
12929	13247		5.7	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylsulphatase protein gene (EDA), exon 2 and flanking repeat regions
12960	28626	31979	2.19	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTO Homo sapiens cDNA clone HTOCNC12 5'
13179	26766		4.71	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2240	13373	28501	0.98	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4820	17757	30739	1.93	8.0E-34	BE092570.1	EST_HUMAN	QV2-BT0288-071288-019-g07 BT0288 Homo sapiens cDNA
7974	21024	34537	0.67	8.0E-34	BE09882.1	EST_HUMAN	MR4-BT0398-200100-001-h03 BT0398 Homo sapiens cDNA
1476	14629	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	yd15c05.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5'
10204	14629	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	yd15c05.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5'
12482	26334		3.85	7.0E-34	H12866.1	EST_HUMAN	y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	26711	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
483	13677	26712	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.58	6.0E-34	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12280	25216	32059	2.22	6.0E-34	U03886.1	NT	Mus musculus DAB/2J hair-specific (hach-1) gene
1928	15072		3.16	5.0E-34	7708500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	19295	31257	5.24	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
9067	22146	35683	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10890	23974	37605	2.02	5.0E-34	AB037656.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11832	24588		1.93	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2054	15195	28309	2.09	4.0E-34	AI804657.1	EST_HUMAN	394c05.x1 NCL CGAP P128 Homo sapiens cDNA clone IMAGE:2248194 3'
3241	18415	29430	0.9	4.0E-34	5803168	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
5981	19166	32486	0.62	4.0E-34	AA881773.1	EST_HUMAN	al35c01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407836 3'
9238	22315	35857	0.63	4.0E-34	BF209778.1	EST_HUMAN	801874950F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6361	19531	32890	0.66	3.0E-34	M87277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11420	24481		2.96	3.0E-34	BF035327.1	EST_HUMAN	801458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
							wd35g06.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to cartilage
9152	22230	35774	0.75	2.0E-34	AI878101.1	EST_HUMAN	MER29.12 MER29 repetitive element;
9152	22230	35775	0.75	2.0E-34	AI878101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to cartilage
11431	24492	38156	8.64	2.0E-34	P51905	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)

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11431	24492	38157	8.54	2.0E-34	P51805	SW/SSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1534	14687	27767	10.13	1.0E-34	P12236	SW/SSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1736	14887		7.18	1.0E-34	AU136024.1	EST_HUMAN	AU136024 PLACET Homo sapiens cDNA clone PLACE1003383 5'
3764	16925	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.79	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.26	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0606-240400-016-H08 BT0608 Homo sapiens cDNA
6266	19440	32787	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
6266	19440	32788	2.26	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
9527	22592	36163	0.54	1.0E-34	P23266	SW/SSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9898	22638	38523	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563.L1 964 (synonym: hfbir2) Homo sapiens cDNA clone DKFZp564A1563 5'
11469	24518	38188	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11469	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12680	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.at NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb.X68203
12950	26660		5.84	1.0E-34	AL163210.2	EST_HUMAN	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3735	16896	29900	1.3	9.0E-35	AW593302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G010
232	13433		7.21	8.0E-35	6031190	NT	HT77b06.yf NCL_CGAP_G01 Homo sapiens cDNA clone IMAGE:2988787 5'
1776	14925	28018	3.63	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1776	14925	28019	3.63	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4989	18118	31097	2.61	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
10299	24011	37645	1.53	8.0E-35	BE378480.1	EST_HUMAN	naa33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
12404	25283		9.99	8.0E-35	BF589282.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
6813	19773	33164	1.61	7.0E-35	11428417	NT	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:404324 5'
1445	14598	27675	1.06	6.0E-35	AA757115.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
2026	15186	28271	4.63	6.0E-35	6005975	NT	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300560 3'
4184	17314	30309	0.8	6.0E-35	AW297191.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
8081	21163	34680	4.03	6.0E-35	6005921	NT	eh53h03.s1 Scarsa, testis, NH-T Homo sapiens cDNA clone 1309397 3'
8006	21985	35524	0.57	6.0E-35	X94232.1	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
							UHL-BWO-ajd-d-09-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
							Homo sapiens triple functional domain (P-TRF interacting) (TRIO), mRNA
							H. sapiens mRNA for novel T-cell activation protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8006	21985	35525	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
8867	22907	36492	0.61	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0368 gene, partial cds
10107	23145	36743	2.97	6.0E-35	AB037786.1	NT	Human mRNA for KIAA1365 protein, partial cds
146	13373	26406	0.61	5.0E-35	AF154630.1	NT	Human sapiens carboxyl phosphate synthetase [mRNA, complete cds]
1746	14893	27989	2.25	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2844	15958	28067	0.99	5.0E-35	AB007866.2	NT	Human sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	29271	2.87	5.0E-35	6912639	NT	Human sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17667	30653	1.72	5.0E-35	AF023268.1	NT	Human sapiens cik2 kinase (CIK2), propin1, cotet1, glucocorticoidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE809992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	gg35c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	gg35c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249 HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-35	BE237907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1662	15008	28114	11.21	4.0E-35	H81193.1	EST_HUMAN	yu88a07.r1 Soares_fetal_liver_spleen_TNFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
7358	20437		1.97	4.0E-35	BE350127.1	EST_HUMAN	h09501.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
8715	21795	35332	8.05	4.0E-35	AL046596.1	EST_HUMAN	MER29 repetitive element ;
12098	25078	38788	2.5	4.0E-35	AF114156.1	NT	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1610	14793	27843	33.92	3.0E-35	BE288182.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
2408	15539		2.64	3.0E-35	AF224492.1	NT	601125280F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
5456	18856	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18856	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
5456	18856	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
6689	22758		1.45	3.0E-35	AF223391.1	NT	Q9QZH7 F-BOX PROTEIN FBL2 ;
10378	23413	37022	1.5	3.0E-35	AW003063.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							wf03a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN
							P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;

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111	16005	26372	1.25	2.0E-35	N88865.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1215	14376	27436	1.89	2.0E-35	T11909.1	EST_HUMAN	REPETITIVE ELEMENT
2262	15424	28558	4.56	2.0E-35	AB018413.1	NT	A971F Human Homo sapiens cDNA clone A971
2748	15955	28976	1.13	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3388	16556	28570	1.08	2.0E-35	6912459	NT	h86a12.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2878166 3' similar to
3388	16556	28571	1.08	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12:
3647	16810		0.77	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17178	30184	0.85	2.0E-35	BE247576.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4019	17178	30185	0.85	2.0E-35	BE247576.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4782	17827		3.01	2.0E-35	H49239.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
5700	18894	32186	1.93	2.0E-35	BF332417.1	EST_HUMAN	MT9a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
7253	20336	33785	0.6	2.0E-35	BE832636.1	EST_HUMAN	QV0-BT0701-2T0400-169-504 BT0701 Homo sapiens cDNA
7253	20336	33786	0.8	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11036	24116	37749	2.93	2.0E-35	X59417.1	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12157	16556	28570	1.22	2.0E-35	6912459	NT	H. sapiens PQS-27 mRNA
12157	16556	28571	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	601498774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898693 5'
12831	25614		7.22	2.0E-35	AL163210.2	NT	601498774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898693 5'
13056	16005	26372	1.74	2.0E-35	N88865.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
47	13286	26286	5.76	1.0E-35	AA631949.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
47	13286	26286	5.76	1.0E-35	AA631949.1	EST_HUMAN	REPETITIVE ELEMENT
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	frf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27001	35.82	1.0E-35	AW389473.1	EST_HUMAN	frf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
932	14107		1.28	1.0E-35	T87947.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2907	15730	28847	1.89	1.0E-35	7705894	NT	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2826	15940	29050	1.34	1.0E-35	BE350127.1	EST_HUMAN	Yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
							SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
							Homo sapiens hypothetical protein LOC51293, mRNA
							h109d01.x1 NCI CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
							MER28 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2928	15940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
3212	16366	29397	1.87	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3232	16406	29418	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
3232	16406	29419	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4542	17680	30661	4.82	1.0E-35	7656805	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4542	17680	30662	4.82	1.0E-35	7656805	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
6627	18821	31896	1.48	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7135	18561	31475	0.74	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111196-011-007 ST0111 Homo sapiens cDNA
7135	18561	31476	0.74	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111196-011-007 ST0111 Homo sapiens cDNA
7652	20720	34196	0.99	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7819	20874	34373	0.91	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
9742	26861	36383	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLAGE3000382 3'
9742	26861	36384	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAGE3 Homo sapiens cDNA clone PLAGE3000382 3'
10805	23838	37462	0.72	1.0E-35	BF595954.1	EST_HUMAN	naa06d08.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3264051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
10805	23838	37463	0.72	1.0E-35	BF595954.1	EST_HUMAN	naa06d08.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3264051 3' similar to TR:O31341 O31341 BETA-GALACTOSIDASE ;
12055	25036	38743	1.49	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12055	25036	38744	1.49	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12062	25043		2.04	1.0E-35	AI525119.1	EST_HUMAN	promina-7 D01.1 bitumor Homo sapiens cDNA 5'
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12405	25284		1.28	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
12806	25539		2.49	1.0E-35	BE792832.1	EST_HUMAN	601394833F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3938986 5'
6131	18310	32650	0.67	8.0E-36	X78479.1	NT	B. bovis BB50 mRNA for schlerin
9430	22504	36070	0.78	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2897	15173	28192	1.53	7.0E-36	AW867579.1	EST_HUMAN	CMT-CT0315-091298-063-d07 CT0315 Homo sapiens cDNA
3188	16363		5.25	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
5273	18392	31360	1.09	7.0E-36	Q27409	SWISSPROT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
7832	20887	34389	6.31	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
7832	20887	34390	6.31	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
12570	23388	32040	27.38	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2060	15201	28315	1.92	6.0E-36	7708822	NT	Homo sapiens hnjunr2 (NINJ2), mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TCE6 gene, exon 12
3729	18850	29894	0.59	6.0E-36	BF515101.1	EST_HUMAN	UHH-BW71-anv-c-12-0-U1.e1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5446	18646	31624	7.17	6.0E-36	AI435169.1	EST_HUMAN	HS3306.X1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33792	3.03	6.0E-36	AW780143.1	EST_HUMAN	hs06h02.X1 NCL CGAP_Cot4 Homo sapiens cDNA clone IMAGE:3036527 3' similar to SW:IMA2_HUMAN
8553	21832	35471	4.52	6.0E-36	AF208161.1	NT	Homo sapiens synchyrin precursor, mRNA, complete cds
10430	23465		0.63	6.0E-36	CT6927.1	EST_HUMAN	CT6927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER8 b2
11841	24830	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	HS9508.X1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3607289 5'
140	13366	26399	15.16	5.0E-36	AJ271735.1	NT	MER8 repetitive element;
2809	19223	29033	21.08	5.0E-36	BE398436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3700	18861	29853	3.24	5.0E-36	AL163209.2	NT	601285567.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4909	18039	31029	1.31	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
7968	21016	34528	0.59	5.0E-36	11070227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12168	13366	26399	6.11	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12458	25322	32095	2.36	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1677	14829	27013	1.36	4.0E-36	BE382574.1	EST_HUMAN	601298574.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2287	15428		4.14	4.0E-36	AW247772.1	EST_HUMAN	2820020.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3435	16603	29622	1.1	4.0E-36	BE389289.1	EST_HUMAN	601282266.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3435	16603	29623	1.1	4.0E-36	BE389289.1	EST_HUMAN	601282266.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4877	18008	30982	0.69	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5533	19024		0.96	4.0E-36	RG4023.1	EST_HUMAN	316105.T1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:139713 5'
6180	19356	32704	2.49	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7831	20896	34388	1.78	4.0E-36	MS3320.1	NT	Human platelet Glycoprotein Iib (GPIIb) gene, exon 2-29
8752	21831	35369	1.45	4.0E-36	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8752	21831	35370	1.45	4.0E-36	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11235	24304	37641	3.13	4.0E-36	AA400370.1	EST_HUMAN	zu89c10.11 Soares testis NHT Homo sapiens cDNA clone IMAGE:743250 5'
12476	25328		1.91	4.0E-36	11420518	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
12520	25951		4.27	4.0E-36	AV753929.1	EST_HUMAN	AV753929 TP Homo sapiens cDNA clone TPGABH01 5'
714	13896	26934	2.63	3.0E-36	AF096810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7662401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus juncophilin 1 (Jp1-pending), mRNA
11368	24429	38096	1.84	3.0E-36	BF035327.1	EST_HUMAN	601458531 F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	18412	29427	2.5	2.0E-36	BE259287.1	EST_HUMAN	601106343 F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
5074	18202	31174	10.78	2.0E-36	AW890376.1	EST_HUMAN	QV6-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5903	18798	31848	2.88	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5970	19166	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST00648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBB.28 5' end
8706	19864	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	Y444a07.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9588	22643	36212	0.94	2.0E-36	BF512794.1	EST_HUMAN	U-H-BW1-aru-a-11-0-U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300938 F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-H1T0217-131195-021-h07 HT0217 Homo sapiens cDNA
2212	19346	28475	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-H1T0217-131195-021-h07 HT0217 Homo sapiens cDNA
2275	15408	28538	1.83	1.0E-36	BF673761.1	EST_HUMAN	602136493 F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:427286 5'
3425	19594		3.33	1.0E-36	AF156962.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5847	19037	32344	0.64	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AI867714.1	EST_HUMAN	wic37c12.x1 NCL_CGAP_GCB Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6519	19684	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	y938g10.r1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6519	19684	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	y938g10.r1 Scores infant brain INIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6820	19973	33381	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1_761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21229	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z551a12.r1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8373	21454	34978	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9228	22307	35850	3.33	1.0E-36	AW103668.1	EST_HUMAN	xe92607.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10320	23355	36964	3.83	1.0E-36	BF384189.1	EST_HUMAN	QV9-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA
10334	23569	37178	0.64	1.0E-36	AW856868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.64	1.0E-36	AW885983.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11190	24259	37895	2.55	1.0E-36	AW887633.1	EST_HUMAN	GM3-NN0081-140400-147-H12 NN0081 Homo sapiens cDNA
11692	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	UHF-BNq-ale-c-03-05-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25029		10.8	1.0E-36	11545901	NT	Homo sapiens PP3227 protein (PP3227), mRNA
12340	25245		2.93	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12835	25556		5.76	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.76	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12619	25417		3.57	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	28624	1.4	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5363	18666		1.7	8.0E-37	BE598077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element ;
5998	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element ;
8088	21160	34870	6.2	8.0E-37	X87344.1	NT	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1313	14469		4.92	7.0E-37	AL042800.1	EST_HUMAN	H.sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
5228	18350	31320	3.04	7.0E-37	AW968823.1	EST_HUMAN	DKFP434E0422_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFP434E0422 5'
10894	24073	37708	8.66	7.0E-37	A1817700.1	EST_HUMAN	EST1380899 IMAGE resequences, MAGJ Homo sapiens cDNA
11134	24206	37831	1.89	7.0E-37	A1536702.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
8634	21714	35251	0.59	6.0E-37	AF189889.1	NT	PTR5 repetitive element ;
12864	25575		2.3	6.0E-37	U78308.1	NT	h08g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1
12884	25641		4.5	6.0E-37	AF202723.1	NT	repetitive element ;
8218	19393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
8218	19393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	Human diffractory receptor olfr17-201-1 (OR17-201-1) gene, diffractory receptor olfr17-32 (OR17-32) gene and olfractory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
11160	24231		4.02	5.0E-37	7667117	NT	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12335	25242		3.63	5.0E-37	AF149773.1	NT	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
							AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
							Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
							Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2495	15622	28741	2.97	4.0E-37	AA702789.1	EST_HUMAN	280b04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	16685	32947	0.68	4.0E-37	AW794502.1	EST_HUMAN	RC6-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9556	22621	36192	0.56	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares parathyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2581	15706		1.64	3.0E-37	AW961150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
3030	16208		4.02	3.0E-37	AW961150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
5985	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067_r1 547 (synonym: hbr1) Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
7728	20790	34278	0.72	3.0E-37	A1749952.1	EST_HUMAN	ak34c05.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
392	13629	26666	0.89	2.0E-37	D89780.1	NT	Q13537 SIMILAR TO POGO ELEMENT. ;
392	13629	26667	0.89	2.0E-37	D89780.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	Homo sapiens mRNA for AML1, complete cds
1105	14270	27329	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28267	1.32	2.0E-37	AL163247.2	NT	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
3998	17156	30162	6.71	2.0E-37	4503210	NT	Homo sapiens chromosome 21 segment HS21C047
4360	17503	30485	0.6	2.0E-37	4826685	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
5504	18703		0.9	2.0E-37	BF036327.1	EST_HUMAN	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6676	18835	33224	0.6	2.0E-37	11690617	NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6788	19953	33553	3.72	2.0E-37	AA346720.1	EST_HUMAN	EST62931 Fetal heart II Homo sapiens cDNA clone IMAGE:3453657 5'
8185	21267	34760	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8185	21267	34791	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12797	26770		1.44	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
13184	25770		4.19	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2164	15290	28417	6.95	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C031
3267	16441		1.03	1.0E-37	AW862062.1	EST_HUMAN	RC3-CT0347-210400-016-H03 CT0347 Homo sapiens cDNA
5055	18163	31158	2.34	1.0E-37	BF371719.1	EST_HUMAN	QY0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6127	19308		0.89	1.0E-37	7306360	NT	Mus musculus otogelin (Otog), mRNA
8409	21460	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	601072416F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
9933	22012	35551	3.59	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1:12 L1 repetitive element ;

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10937	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12871	25447		1.94	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0086-140700-243-c07 FT0086 Homo sapiens cDNA
5898	19086	32398	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Plocado (LOC56766), mRNA
1248	14408	27470	1.96	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIA00571), mRNA
2597	15692	28817	1.21	8.0E-38	BF348221.1	EST_HUMAN	602018401FT101 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153982 5'
12735	14408	27470	1.37	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIA00571), mRNA
13210	26048		1.44	8.0E-38	AB002039.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	18387	28515	1.7	7.0E-38	AW972823.1	EST_HUMAN	EST384920 IMAGE resequences, MAGL Homo sapiens cDNA
3107	16283	29299	1.98	6.0E-38	BF033033.1	EST_HUMAN	601456722FT NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859348 5'
5706	18993	32192	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5708	18998	32193	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20557	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002039.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31861	1.79	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13526	28987	0.9	5.0E-38	AW971819.1	EST_HUMAN	EST383903 IMAGE resequences, MAGL Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3799	16957	29981	0.94	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3971	16957	29981	0.77	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5288	15650	28774	0.99	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
7172	20505	33748	1.83	5.0E-38	BE671610.1	EST_HUMAN	601450148FT NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3854074 5'
121	13351	26380	4.25	4.0E-38	Z25468.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z25468.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14946	27403	1.15	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
2167	15302		4.42	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnA-like) (HIRIP4), mRNA
3958	17116	30119	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4738	17871		0.81	3.0E-38	BE276301.1	EST_HUMAN	601157533F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6893	25838	33463	5.99	3.0E-38	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7333	20471	33937	0.58	3.0E-38	AV302461.1	EST_HUMAN	xx04d01.x1 NCI CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2827009 3'
7763	20822	34373	6.53	3.0E-38	BF373684.1	EST_HUMAN	CM3-FT0181-140700-241-c07 FT0181 Homo sapiens cDNA
8851	21930	34469	2.11	3.0E-38	H85484.1	EST_HUMAN	y88b04.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'
8831	21930	35470	2.11	3.0E-38	H85484.1	EST_HUMAN	y88b04.1 Scores melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:249775 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24651		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
61	13290	26303	1.96	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14565	27639	3.66	2.0E-38	5902007	NT	Homo sapiens SMT3 (suppressor of mit w/o 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	z30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	z30d01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3622	16798		0.92	2.0E-38	AF070670.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17839	30824	15.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5252	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	z30d01.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:3817957
5836	19026	32331	0.78	2.0E-38	Z28634.2	NT	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5836	19026	32332	0.75	2.0E-38	Z28634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20949	34457	1.47	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8680	21760		4.47	2.0E-38	BE165980.1	EST_HUMAN	MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA
9096	22178	35719	0.49	2.0E-38	F06450.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9165	22243	35786	1.26	2.0E-38	AF069756.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22466		1.36	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NO1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168130 3' similar to TR:002710 C02710
10665	23699	37309	1.67	2.0E-38	D63479.2	NT	GAG POLYPROTEIN ;
11781	24771	38467	4.86	2.0E-38	BE712790.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11939	24925	38826	2.86	2.0E-38	AF190501.1	NT	QV2-HT0698-080800-293-e05 HT0698 Homo sapiens cDNA
11939	24925	38827	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25186		6.21	2.0E-38	AV726988.1	EST_HUMAN	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12246	25187		1.26	2.0E-38	AB012723.1	NT	AV726988 HTC Homo sapiens cDNA clone HTCAHX-07 5'
12546	25370		3.36	2.0E-38	M55630.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12559	25381	32073	4.81	2.0E-38	H55641.1	EST_HUMAN	Human topoisomerase I pseudogene 2
12632	25426		2.87	2.0E-38	S74906.1	NT	CHR220560 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13174	25702		1.35	2.0E-38	11418248	NT	ET beta-pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt]
							Homo sapiens sulfoxidase-related protein (SUL TX3), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.98	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
2055	15193	28310	2.52	1.0E-38	4885283	NT	MER19 repetitive element ;
2077	15217	28336	1.33	1.0E-38	7661963	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2864	15088	28815	1.89	1.0E-38	AF270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4271	17416	30406	0.83	1.0E-38	AB037863.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
							Homo sapiens mRNA for KIAA1442 protein, partial cds
4439	17579	30568	0.6	1.0E-38	4506018	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30537	1.08	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5268	18387	31365	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6151	18327	32872	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6151	18327	32873	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
7563	20635	34110	2.55	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
9354	22429	35987	0.58	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9810	22665	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148285 3' similar to contains MER29.b3
12403	25877		4.79	1.0E-38	AL163284.2	NT	MER29 repetitive element ;
12116	25086	38801	1.84	8.0E-39	AA112438.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
55	13294	26309	4.93	8.0E-39	4502312	NT	znt2707.r1 Stratagene pancreas (#837208) Homo sapiens cDNA clone IMAGE:526885 5'
1425	14579	27652	1.3	8.0E-39	4758223	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) T680 (ATP6C) mRNA
							Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1878	16020		1.8	8.0E-39	AB23404.1	EST_HUMAN	wh58f10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
2160	15298	28421	7.08	7.0E-39	AL163227.2	NT	POL PROTEIN ;
11047	24124	37758	2.4	6.0E-39	BF331829.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
13064	25697		2.24	6.0E-39	BE670394.1	EST_HUMAN	QV1-BT0831-040800-357402 BT0831 Homo sapiens cDNA
							7e34c03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R161.6
							CE00828 ;
1032	14201	27269	1.84	5.0E-39	AF003528.1	NT	Homo sapiens X-linked aryliditol oxidase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3950	16228	28247	9.33	5.0E-39	A1750154.1	EST_HUMAN	ad26b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374083 3' similar to TR:Q15408
12720	25479		1.53	6.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.H LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
584	13766	26782	4.39	4.0E-39	AB015610.1	NT	Chloroebus aethiops mRNA for ribosomal protein S4X, complete cds
3663	16826	29835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	19136	32450	0.8	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5950	19136	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene echtozo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains ORF.b1 ORF repetitive element
9330	22595	36165	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9330	22595	36166	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494		6.36	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12884	25598		2.56	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-006 FN0063 Homo sapiens cDNA
48	13287	26297	11.98	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26298	11.96	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26299	11.96	3.0E-39	AA631949.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25180	38348	6.59	3.0E-39	A084557.1	EST_HUMAN	ox63a10.s1 Scores_NHMPu S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12236	25180	38349	6.59	3.0E-39	A084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE
12284	25212		5.72	3.0E-39	H37903.1	EST_HUMAN	ye51c06.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
920	14095		7.78	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
935	14110		11.55	2.0E-39	A1525119.1	EST_HUMAN	promma-7.D01.r bvtumor Homo sapiens cDNA 5'
1057	14223		3.9	2.0E-39	AF000573.1	NT	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
1560	14713		33.59	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT0340-211298-003-402 BT0340 Homo sapiens cDNA
2030	15171	28279	4.48	2.0E-39	AA720574.1	EST_HUMAN	nv21g02.s1 NCL_CGAP_GC50 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element
2692	15812	28928	1.89	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4523	17682	30649	1.74	2.0E-39	BF370207.1	EST_HUMAN	RCA-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
5608	18803	31868	4.45	2.0E-39	AA508880.1	EST_HUMAN	ng6803.s1 NCL_CGAP_PB Homo sapiens cDNA clone IMAGE:941693
7626	20599	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	zn0502.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
7702	20767	34251	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7702	20767	34252	0.88	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8505	21586	35120	0.63	2.0E-39	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9826	22866		0.79	2.0E-39	A0686660.1	EST_HUMAN	tu35a03.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253052 3'
11716	24756	39452	2.13	2.0E-39	D86994.1	NT	Human mRNA for KIAA0209 gene, partial cds
1543	14695	27774	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQ11 gene

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1543	14695	27775	2.83	1.0E-39	AJ008345.1	NT	Homo sapiens KVLQT1 gene
1661	14714	27791	5.96	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1783	14912	28007	1.14	1.0E-39	H65224.1	EST_HUMAN	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17917	30903	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGEB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGEB Homo sapiens cDNA
4824	17957	30943	6.13	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5474	18973	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18973	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	Alu repetitive element: contains LTR1 repetitive element;
6781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6965	20163		1.85	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7621	20594	34089	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35392	1.04	1.0E-39	O46630	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11165	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 60kD, polypeptide 5 (RPS6KA5) mRNA
669	13761	28785	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4755146	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1263	14420	27485	16.02	9.0E-40	4755146	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3885	17044	30043	1.18	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4466	17606	30564	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3106	16282	29258	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HLA cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17168		3.43	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC: 8 Homo sapiens cDNA clone IMAGE:3619186 5'
7694	20946	34462	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7694	20946	34463	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	15904	29011	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2788	15904	29012	9.91	6.0E-40	AA361276.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6060	19242		1.85	6.0E-40	BE504783.1	EST_HUMAN	h49g01.x1 NCL CGAP_GG6 Homo sapiens cDNA clone IMAGE:3210480 3'
6275	19449		1.38	6.0E-40	7661989	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7075	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10182	23219	36812	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2670	15791	28907	2.75	6.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1925	15068	28173	3.91	4.0E-40	A1686005.1	EST_HUMAN	h91b01.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN, ;
2175	15310		6.91	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17647	30635	7.2	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.94	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	hV34e10.r1 NCL CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10955	24036	37671	1.95	4.0E-40	AW841586.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17368	30385	0.9	3.0E-40	A1925949.1	EST_HUMAN	h1207.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:377163 3'
4993	18122		0.83	3.0E-40	AA055118.1	EST_HUMAN	z16h09.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:377163 3'
8592	19762	33137	0.66	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6777	19932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.86	3.0E-40	5464167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	22247	35790	1.27	3.0E-40	AF076779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22486	36050	1.6	3.0E-40	AF076779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D86864.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24600	38276	9.12	3.0E-40	6006813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	A123036.1	EST_HUMAN	q952h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13996		5.58	2.0E-40	AW303868.1	EST_HUMAN	h22e10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 4PS RIBOSOMAL PROTEIN S6. ;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731801.1	EST_HUMAN	AV731801 HTF Homo sapiens cDNA clone HTFAZE05 5'
1888	15130	28233	2.8	2.0E-40	4508188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1888	15130	28234	2.8	2.0E-40	4508188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15269	28389	1.39	2.0E-40	AI963592.1	EST_HUMAN	w60a11.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2614716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
2238	15371	28500	2.21	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
2754	15971	28500	1.66	2.0E-40	BE276932.1	EST_HUMAN	501121597F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3108	16371	28378	5.27	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
908	14081		1.2	1.0E-40	AA225989.1	EST_HUMAN	nc09q09.s1 NCL CGAP_P71 Homo sapiens cDNA clone IMAGE:1007608
2886	15806	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	501460375F1 NIH_MGC_06 Homo sapiens cDNA clone IMAGE:3863803 5'
2750	15897		3.88	1.0E-40	BE018348.1	EST_HUMAN	5b79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92158 Q92158 SYNTAXIN 17. ;
3370	16542		2.14	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4733	17868	30851	3.69	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6385	18594	32912	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6385	18594	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42804.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	nj42804.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7381	20459	33922	0.82	1.0E-40	P28808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
11157	24228	37858	6.41	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11993	24978	38683	1.49	1.0E-40	AA614255.1	EST_HUMAN	np09h03.s1 NCL CGAP_P73 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136406
11993	24978	38684	1.49	1.0E-40	AA614255.1	EST_HUMAN	G1136406 KIAA0173 PROTEIN. ;
12078	25069		1.86	1.0E-40	AL163246.2	NT	np09h03.s1 NCL CGAP_P73 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136406
12887	26032		6.94	1.0E-40	BF334712.1	EST_HUMAN	G1136408 KIAA0173 PROTEIN. ;
3006	17065	30064	0.59	9.0E-41	W01566.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
8106	21188	34708	1.8	8.0E-41	AL163203.2	NT	MPK2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
851	18024	27059	2.52	7.0E-41	AI934384.1	EST_HUMAN	2a35602.11 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:294602 5'
851	18024	27059	2.52	7.0E-41	AI934384.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
851	18024	27059	2.52	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
851	18024	27059	2.52	7.0E-41	AI934384.1	EST_HUMAN	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5379	18581	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypodermal protein FLJ13188 (FLJ13188), mRNA
6132	19311	32651	2.71	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAMP22), mRNA
6483	19650	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LJS1) gene, exons 3 and 4
11718	24758	38453	2.06	7.0E-41	4759445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
11931	24917	38620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028	26543	8.58	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	6.0E-41	AB037163.1	NT	Homo sapiens DSCR85 mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8155	21240	34760	1.31	6.0E-41	BF513783.1	EST_HUMAN	U1H-BW1-amp-b-03-0-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13156	25952		1.25	6.0E-41	AW873637.1	EST_HUMAN	nc6408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains
1845	14991	28092	1.37	5.0E-41	T62628.1	EST_HUMAN	MER32.b3 MER32 repetitive element;
4225	17371		1.17	5.0E-41	4886639	NT	yc03e10.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:79626 3'
6676	19837		2.34	5.0E-41	BE087042.1	EST_HUMAN	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
402	13599		1.69	4.0E-41	BE156318.1	EST_HUMAN	PM4-BT0341-251199-002-F1.1 BT0341 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU119344.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
							AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
1442	14595	27670	14.6	4.0E-41	A1027117.1	EST_HUMAN	qw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
							TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. contains LTR5.b1 LTR5 repetitive element;
1442	14595	27871	14.6	4.0E-41	A1027117.1	EST_HUMAN	qw45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
1454	14607	27687	3.34	4.0E-41	AB008681.1	NT	TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. contains LTR5.b1 LTR5 repetitive element;
							Homo sapiens gene for activin receptor type IIB, complete cds
1665	14817	27900	7.72	4.0E-41	AI500406.1	EST_HUMAN	tn98e04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1
2963	16130	29144	5.02	4.0E-41	AJ229041.1	NT	OFR repetitive element;
2953	16130	29145	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4262	17407	30393	2.13	4.0E-41	X92695.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6638	18797		1.8	4.0E-41	AV758295.1	EST_HUMAN	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
9935	22835	36519	5.06	4.0E-41	BF304693.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
11989	24954		7.38	4.0E-41	AV710480.1	EST_HUMAN	80188809F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
							AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
13110	25725	31942	1.51	4.0E-41	BE887118.1	EST_HUMAN	601503315F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3910059 5'
870	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4455	17595	30575	4.03	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5609	18804	31869	11.78	3.0E-41	XB7689.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6511	19678	33046	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7967	21017	34528	0.71	3.0E-41	R54765.1	EST_HUMAN	Y75408.1 Soares breast 2NpHbSt Homo sapiens cDNA clone IMAGE:154575 5'
12119	25099	38804	1.36	3.0E-41	AW994841.1	EST_HUMAN	QY0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12119	25099	38805	1.36	3.0E-41	AW994841.1	EST_HUMAN	QY0-BN0040-170300-160-h08 BN0040 Homo sapiens cDNA
12196	25153		1.98	3.0E-41	AA609768.1	EST_HUMAN	af17110.1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25526		1.43	3.0E-41	BF125922.1	EST_HUMAN	601782940F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:4026081 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15163	28258	2.17	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2293	15425	28559	1.26	2.0E-41	D68962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28806	5.52	2.0E-41	X69831.1	NT	G. gallus DNA for ZNF80 gene homolog
2889	14744	27827	11.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16578	29591	0.69	2.0E-41	AA449549.1	EST_HUMAN	z08b04.r1 Soares total testis_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:785839 5'
3841	17100	30097	0.69	2.0E-41	5032103	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17879	30862	1.23	2.0E-41	AL183267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17879	30863	1.23	2.0E-41	AL183267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5656	18850	32132	0.6	2.0E-41	AA584576.1	EST_HUMAN	nc12e07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:X52851.1na1
6763	19919	33314	0.98	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7850	20905	34409	9.27	2.0E-41	AFC38404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8269	21341	34868	1.36	2.0E-41	M96944.1	NT	Homo sapiens homolog of Nedd5 (Nedd5) mRNA, complete cds
8269	21341	34869	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8288	21370	34891	1.42	2.0E-41	AA328285.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9175	22263	35766	1.65	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9017	22672	36241	0.66	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11775	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
13148	25747		1.2	2.0E-41	11420516	NT	EST184565 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3276	19450	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	18450	29471	1.05	1.0E-41	BE669735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17824	30811	9.48	1.0E-41	6078488	NT	Mus musculus tubulin alpha 6 (Tub6), mRNA
9618	22673	36243	1.57	1.0E-41	AI217888.1	EST_HUMAN	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1758898 3'
12334	25241		1.67	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9375	22450	36011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22604 (FLJ22604), mRNA
9375	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22604 (FLJ22604), mRNA
475	13670	26702	5.34	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2176	15311	28439	8.53	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12375	26035		30.09	8.0E-42	AA463896.1	EST_HUMAN	h07c02.st NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943588 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA;
12396	25904		2.91	8.0E-42	AW088092.1	EST_HUMAN	xc97a04.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12 OFR repetitive element;
955	14128		2.23	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8666	21746		0.5	7.0E-42	R10963.1	EST_HUMAN	y38g04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
9445	22561	36124	1.32	7.0E-42	AI204359.1	EST_HUMAN	q58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2363	15494		3.6	6.0E-42	AW238656.1	EST_HUMAN	xp28f08.x1 NCL_CGAP_JH10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.L1 repetitive element;
5584	18779	31824	1.65	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5834	18779	31824	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
138	13364		8.34	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
451	13647	26683	1.56	5.0E-42	BE217913.1	EST_HUMAN	h03e11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
489	13694		3.05	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
500	13695		1.14	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6825	19978	33365	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6825	19978	33369	0.94	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6941	20264	33691	2.57	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7351	20430	33892	1.55	5.0E-42	AF071589.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	22057	35599	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431108	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431108	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24315	37657	1.77	6.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class I region
772	13953	27003	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class I region
1091	14256	27312	1.82	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3), mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4343	17488	30489	1.1	4.0E-42	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4364	17507	30488	4.87	4.0E-42	4506466	NT	Homo sapiens zinc finger protein 177 (ZNF177), mRNA
4706	17841	30825	17.64	4.0E-42	4508008	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
5285	18404	31372	0.93	4.0E-42	4508008	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	CMO-BT0282-171289-127-503 BT0282 Homo sapiens cDNA
10884	23968	37697	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10884	23968	37698	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AI435225.1	EST_HUMAN	ifl1d02.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24935	38387	1.69	4.0E-42	BF036327.1	EST_HUMAN	601458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1512	14955	27750	3.79	2.0E-42	BF78834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2466	15693	28718	1.6	2.0E-42	AV990218.1	EST_HUMAN	AV990218 GKC Homo sapiens cDNA clone GKGB08 5'
2483	19510		4.24	2.0E-42	AW888344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2496	19523	28742	3.6	2.0E-42	AW250059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5875	19065	32372	11.82	2.0E-42	AW655368.1	EST_HUMAN	EST367438 MAGE resequences, MAGE Homo sapiens cDNA
5875	19065	32373	11.82	2.0E-42	AW655368.1	EST_HUMAN	EST367438 MAGE resequences, MAGE Homo sapiens cDNA
6892	20044	33452	0.9	2.0E-42	AI052586.1	EST_HUMAN	bw83d05.x1 Soares_Fetal_liver_spleen_TNFSL_ST Homo sapiens cDNA clone IMAGE:1663417 3'
10046	23084	36585	1.28	2.0E-42	BE538919.1	EST_HUMAN	501061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23265	36892	0.84	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10260	23265	36893	0.84	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
12037	25019	38725	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
762	19332	26677	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus PHE-1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW295809.1	EST_HUMAN	UI-H-B1-afh-e-04-0-J1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14290	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14290	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	18033	27498	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NAD1-lubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

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1271	16033	27489	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1735	14884	27977	1.15	1.0E-42	11423219	NT	encoding mitochondrial protein, complete cds
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens rec (LOC51201), mRNA
2609	15733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens PDNPI gene, exon 17
3029	16205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3789	16990	29964	3.31	1.0E-42	7662027	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3895	17054	30054	1.11	1.0E-42	5031610	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4036	17192	30202	0.98	1.0E-42	AL163267.2	NT	Homo sapiens Gdgl vesicular membrane trafficking protein p18 (BET1) mRNA
4361	17504	30496	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C087
4716	17851	30834	0.61	1.0E-42	AW813617.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
4867	18000	30884	2.37	1.0E-42	5803122	NT	RC3-ST0197-161099-072-e03 ST0197 Homo sapiens cDNA
4867	18000	30985	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4901	18031	31020	6.13	1.0E-42	4506758	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
11440	24501	38169	1.39	1.0E-42	BE408811.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
10291	23326	36929	8.16	9.0E-43	4757969	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
669	13855	26863	20.77	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
669	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26938	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
5816	19006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	j08e11.1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:148172 5'
3731	16892	29896	7.48	7.0E-43	AW246442.1	EST_HUMAN	2922251:5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8968	22047		3.98	7.0E-43	AB36748.1	EST_HUMAN	wf69b01.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
1374	14529		11.62	6.0E-43	AA491690.1	EST_HUMAN	O16475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
2857	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	ns72d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:309803 similar to gb:U05095 60S
4863	18092	31068	252.27	6.0E-43	A1421540.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6441	19608	32871	2.53	6.0E-43	9956973	NT	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
							tf26c04.x1 NCL_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2097318 3' similar to SW:BRR2_YEAST
							P32639 PRE-MRNA SPLICING HELICASE BRR2 ;
							Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA

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7048	20101	33518	1.8	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2610891 3' similar to contains MER1.13 MER1.MER1 repetitive element ;
10095	23094	36696	1.77	6.0E-43	AA195154.1	EST_HUMAN	z35606.r1 Soares_NHMPUL_S1 Homo sapiens cDNA clone IMAGE:065410 5' similar to TR:G529641
11363	24424		2.45	6.0E-43	AL119158.1	EST_HUMAN	G529841 DB1, COMPLETE CDS, contains element P TR7 repetitive element ;
145	13370		1.82	6.0E-43	AL163213.2	NT	DKFZp761L1712.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761L1712 5'
515	13706	26736	3.4	6.0E-43	AA382780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2908	16086	29100	1.59	6.0E-43	AV732578.1	EST_HUMAN	EST196033 Testis 1 Homo sapiens cDNA 5' end
6435	20096	33512	0.9	6.0E-43	AI613508.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
7043	20096	33512	0.69	6.0E-43	AI613508.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2260452 3'
8381	21462	34985	0.84	6.0E-43	AA442271.1	EST_HUMAN	tw22607.x1 NCI_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2260452 3'
8391	21462	34986	0.64	6.0E-43	AA442271.1	EST_HUMAN	z354603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22169		0.73	6.0E-43	H74277.1	EST_HUMAN	z354603.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9564	22706	36272	4.08	6.0E-43	AA465288.1	EST_HUMAN	y448912.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:226510 5'
10608	23643	37251	2.6	6.0E-43	AI733244.1	EST_HUMAN	aa33408.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:15055 5'
10851	23695	37295	1.02	6.0E-43	ALD49110.1	EST_HUMAN	co52e10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569610 3' similar to TR:P90591 P90591
11001	24080	37715	4.53	6.0E-43	AW863007.1	EST_HUMAN	PV14 GENE ;
11213	24282	37021	2.24	6.0E-43	W29011.1	EST_HUMAN	DKFZp434D0119.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
985	15987	27227	4.4	6.0E-43	AF003528.1	NT	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA
5373	18576	31444	1.09	6.0E-43	AI056335.1	EST_HUMAN	5584 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8489	19665	33028	0.68	6.0E-43	8996008	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7280	20363		1.6	6.0E-43	11418783	NT	cy47n03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1659013 3'
8371	21462	34975	5.18	6.0E-43	AI244341.1	EST_HUMAN	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
8371	21452	34976	5.18	6.0E-43	AI244341.1	EST_HUMAN	Homo sapiens protodactilin beta 6 (PDDH66), mRNA
10521	23556	37164	1.02	6.0E-43	6009507	NT	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
12311	25227		2.7	6.0E-43	R20950.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
13030	25898		1.33	6.0E-43	AI436093.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element ;
							HP0805.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
							th92b12.x1 Soares_NSF_P8_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:212611 3' similar to TR:O02710 O02710 GAG POLYPROTEIN ;

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1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14690	27971	2.52	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
2120	16055	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp8201.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183948 5' similar to contains MSR1 repetitive element;
3662	16825	29834	1.22	3.0E-43	S68002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein [rearranged translocation] [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4405	17548	30532	0.9	3.0E-43	AA548164.1	EST_HUMAN	nk65d06.s1 NCI CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6014	19198	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	19654	33018	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
8487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
8867	20019	33428	5.08	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa8811.1 St1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
9020	22099	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10068	23106	36709	0.68	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63948), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
188	13410		7.24	2.0E-43	AI190764.1	EST_HUMAN	gd61 c09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13
6604	19764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element;
6604	19764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI CGAP_Bim41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
7426	20503	33973	1.29	2.0E-43	AW207390.1	EST_HUMAN	hu53a08.x1 NCI CGAP_Bim41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
8603	21584		3.16	2.0E-43	U43701.1	NT	UI-H-B11-af1-a-08-QJ1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
11476	24635		4.75	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1681	14833	27917	2.96	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stragene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1681	14833	27918	2.96	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27985	4.12	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2766	15902	29000	4.73	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5526	18723	31740	0.88	1.0E-43	4885544	NT	602022313F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4157666 6'
6744	19800	33291	6.84	1.0E-43	4507168	NT	Homo sapiens Pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19800	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
7106	18533	31488	1.19	1.0E-43	R19761.1	EST_HUMAN	y40601.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
8117	21189	34720	0.6	1.0E-43	AF15285.1	NT	SP:BD38_MOUSE P28858 BRAIN PROTEIN DN88 ;
8258	21338		2.17	1.0E-43	AF198460.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
9037	22116	36859	28.54	1.0E-43	AW963675.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
10498	23533	37143	0.68	1.0E-43	AW953229.1	EST_HUMAN	EST375749 IMAGE resequences, MAGB Homo sapiens cDNA
11208	24275	37812	5.31	1.0E-43	A1884981.1	EST_HUMAN	EST365299 IMAGE resequences, MAGB Homo sapiens cDNA
11847	24726	38418	3.05	1.0E-43	11424378	NT	wt87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2484705 3'
12248	25189		2.29	1.0E-43	AL137984.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12550	25373	32071	3.16	1.0E-43	A1675416.1	EST_HUMAN	DKF2p761D1015.r1.761 (synonym: ham2) Homo sapiens cDNA clone DKF2p761D1015 5'
12805	25538	32013	3.21	9.0E-44	11418322	NT	W595b04.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
913	14088	27163	5.32	8.0E-44	A1222985.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	14088	27164	5.32	8.0E-44	A1222985.1	EST_HUMAN	q123g01.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8736	21815	35350	2.89	8.0E-44	X84354.1	NT	q123g01.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1845552 3'
10545	23580	37189	0.5	8.0E-44	11423497	NT	H. sapiens DNA for Cone cGMP-PDE gene
10545	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38164	2.87	8.0E-44	Y10496.2	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11887	24972	38877	1.76	8.0E-44	L29139.1	NT	Homo sapiens mRNA for thymidine kinase, partial
12801	25345	32055	2.89	8.0E-44	11527389	NT	Homo sapiens myosin mRNA, partial cds
12544	25735	31946	2.17	8.0E-44	11418086	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12945	25938	31760	1.85	8.0E-44	11418089	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
13128	25735	31948	2.29	8.0E-44	11418086	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
676	13892		1.13	7.0E-44	R06035.1	EST_HUMAN	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
2307	15439	28573	1.19	7.0E-44	5031836	NT	y88901.1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124920 5'
3031	16207	29228	4.44	7.0E-44	AF048729.1	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3965	17123	30128	2.71	7.0E-44	AL163284.2	NT	Homo sapiens minisatellite ms32 repeat region
4358	17499	30478	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 segment HS21C084
4358	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21480	34893	2.39	7.0E-44	AU169839.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
6229	19404	32754	0.67	6.0E-44	AJ289860.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000498 3'
314	13530		4.25	5.0E-44	AJ289860.1	NT	HSAAADEYU P, Human foetal Brain Whole tissue Homo sapiens cDNA
342	13563		2.42	5.0E-44	AJ289860.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene

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8072	21154	34673	4.12	5.0E-44	AI568523.1	EST_HUMAN	h40d02.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1
9884	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3501	10668	29678	4.27	4.0E-44	AL163303.2	NT	Human sapiens chromosome 21 segment HS21C103
5128	19263		0.99	4.0E-44	AI435225.1	EST_HUMAN	h17d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
7639	20708	34187	0.87	4.0E-44	BE883178.1	EST_HUMAN	607508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910182 5'
8468	21647	35077	0.98	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
8079	22158		0.71	4.0E-44	BE176618.1	EST_HUMAN	RC3-H1T0585-010400-023-008 HT0585 Homo sapiens cDNA
11513	24570	38247	5.64	4.0E-44	U60878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1827	14976		1.5	3.0E-44	6012477	NT	Homo sapiens karyopherin alpha 6 (Importin alpha 7) (KPNA6), mRNA
3167	16342	29350	5.11	3.0E-44	AA168851.1	EST_HUMAN	zp18b05.t1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608777 5'
7970	21020	34533	0.65	3.0E-44	BE884820.1	EST_HUMAN	607510647F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
9719	22784	36355	0.63	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1074	14240	27286	1.43	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1074	14240	27287	1.43	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14393	27455	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1340	14496	27598	6.82	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182988 3' similar to SW:OXYB_HUMAN
2219	15353	28484	3.07	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2605	15726		1.26	2.0E-44	4507592	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2642	15766	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2676	15796		2.3	2.0E-44	5901833	NT	Human mRNA for integrin alpha subunit, complete cds
3558	18724	29740	1.34	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (GLAPS4), mRNA
4992	17827	30813	1.75	2.0E-44	AW864378.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6220	19395	32744	1.75	2.0E-44	11449901	NT	PM4-SN0016-120500-003-004 SN0016 Homo sapiens cDNA
							Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6998	18515	31507	2.18	2.0E-44	AF038968.1	NT	Homo sapiens general transcription factor 2-J (GTF2J) mRNA, alternatively spliced product, complete cds
7572	20644	34121	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7572	20644	34122	3.8	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
8819	21898	35437	1.8	2.0E-44	BE389058.1	EST_HUMAN	607285914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613588 5'

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12152	25122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2789 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2789
12730	26064		1.56	2.0E-44	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
63	13292	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Missipen/NIK-related kinase (MINK), mRNA
53	13292	26307	5.24	1.0E-44	7657334	NT	Homo sapiens Missipen/NIK-related kinase (MINK), mRNA
594	13784	26804	1.93	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-M12 CT0249 Homo sapiens cDNA
1224	14384		1.96	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-B01 BN0039 Homo sapiens cDNA
1605	14758		8.08	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
2209	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53002.r1 Soares_t01_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element
2289	15431	28564	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53002.r1 Soares_t01_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element
2818	15932	29043	1.74	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
3819	18978		3	1.0E-44	AA455869.1	EST_HUMAN	aa01c08.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5221	18343	31314	0.88	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.88	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAG.1 Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequences, MAG.1 Homo sapiens cDNA
8948	21827	35466	0.96	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.56	1.0E-44	A1337183.1	EST_HUMAN	q88g07.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:200628 3'
11284	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11820	24809	38505	3.47	1.0E-44	10082864	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A8.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4701	17836	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4701	17836	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6787	19842	33340	1.41	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	19315	31283	9.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-45	AA377985.1	EST_HUMAN	EST60893 Synovial sarcoma Homo sapiens cDNA 5' end
1583	14735		2.36	6.0E-45	AI075425.1	EST_HUMAN	W889c06.x1 NCL_CGAP_F128 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.11 L1 repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12911	26154		1.89	6.0E-45	11418273	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
915	14080		1.71	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2058	15199	28313	4.42	5.0E-45	BF333627.1	EST_HUMAN	C14-NCN0044-180200-515-91 CN0044 Homo sapiens cDNA
3281	15455	29477	2.87	5.0E-45	AI523766.1	EST_HUMAN	ig94107.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
5929	18823	31897	8.95	5.0E-45	AA387781.1	EST_HUMAN	P09084 PAIRED BOX PROTEIN PAX-1 ;
6143	19321	32864	1.09	5.0E-45	Y18933.1	NT	AT22403.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6143	19321	32665	1.08	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19366	32714	0.92	5.0E-45	AB022318.1	NT	Homo sapiens MCP-1 gene and enhancer region
6190	19366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19490	32847	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6318	19490	32848	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8471	21562	35082	1.12	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9241	22318	35861	1.45	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11997	24982	38888	2.5	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1167	14330	27385	6.3	4.0E-45	X95826.1	NT	H. sapiens ART4 gene
2365	15496	28622	2.15	4.0E-45	BE266622.1	EST_HUMAN	601184440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9157	22235		0.81	4.0E-45	AA226220.1	EST_HUMAN	repetitive element ;
12166	26089	31659	1.36	4.0E-45	11435847	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3411	16580		0.93	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 7NLS Homo sapiens cDNA clone IMAGE:110245 5'
4199	16580		1.03	3.0E-45	T71480.1	EST_HUMAN	y435f07.r1 Soares fetal liver spleen 7NLS Homo sapiens cDNA clone IMAGE:110245 5'
6366	19536	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
6366	19536	32896	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA
8945	21725	35610	1.76	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8991	22070	35610	4.31	3.0E-45	4798451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2), mRNA
10515	23550	37169	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10515	23550	37169	7.52	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2572	16697		3.12	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3097	16273	29287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

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6651	19810	33198	5.45	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7788	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC. 87 Homo sapiens cDNA clone IMAGE:3670838 5'
8610	21690	35228	0.91	2.0E-45	AW634834.1	EST_HUMAN	RCO-L70001-150200-032-d11 L70001 Homo sapiens cDNA
9784	22824	36402	0.51	2.0E-45	A1636766.1	EST_HUMAN	ts56a01.x1 NCL_CGAP_K148 Homo sapiens cDNA clone IMAGE:2232652 3'
11042	25867	37764	12.66	2.0E-45	BE934350.1	EST_HUMAN	MFQ-H10923-190800-201-a02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa8712.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11794	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	TR-G1144569 G1144569 R-SLY1. ;
11794	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745888 3'
13087	25710		2.73	2.0E-45	11418187	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
128	13617		1.22	1.0E-45	BE389655.1	EST_HUMAN	601284360F1 NIH_MGC. 44 Homo sapiens cDNA clone IMAGE:3608183 5'
422	13617		1.99	1.0E-45	BE389655.1	EST_HUMAN	601284360F1 NIH_MGC. 44 Homo sapiens cDNA clone IMAGE:3608183 5'
488	13679	26714	1.02	1.0E-45	4508412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1201	14363	27423	1.66	1.0E-45	U32186.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3172	16347	28354	10.41	1.0E-45	U32186.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3581	16748	29784	0.85	1.0E-45	8695958	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3694	16827	29836	0.69	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4599	17736	30716	6.4	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC. 8 Homo sapiens cDNA clone IMAGE:3616803 5'
4848	17981		1.06	1.0E-45	H57443.1	EST_HUMAN	Y05502.1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:204363 5'
5081	18209	31181	1.59	1.0E-45	11545798	NT	Homo sapiens ribon protein (NIBAN), mRNA
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8806	21885	35425	0.9	1.0E-45	D87675.1	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9321	22897	35950	3.92	1.0E-45	BE887843.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9722	22787	36358	0.99	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12369	25263	32117	3.5	1.0E-45	11416098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12582	25384		19.43	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12588	25387		6.42	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
13047	25066	31963	4.02	1.0E-45	11418167	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8423	21504	35037	2.71	9.0E-46	9910283	NT	Nlus musculus keratin complex 2, gene 6g (Krt-6g), mRNA
8835	21914		6.82	9.0E-46	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C009
10897	23730	37335	6.89	9.0E-46	AW246964.1	EST_HUMAN	2822449.5prime NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2822449 5'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI433261.1	EST_HUMAN	h32908.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
2513	15639	28761	7.67	8.0E-46	AI433261.1	EST_HUMAN	h32908.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);
8244	21328		2.72	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012.C12.H10506 Homo sapiens cDNA
4703	17838		4.79	7.0E-46	BE386163.1	EST_HUMAN	h01277282F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	RC4-B10310-110300-015-f10 B10310 Homo sapiens cDNA
6187	19343	32689	4	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6823	19783	33171	1.8	7.0E-46	BF108045.1	EST_HUMAN	h01822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042735 5'
12706	25469		2.6	7.0E-46	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21CQ46
2812	15926	29037	6.87	6.0E-46	AI884381.1	EST_HUMAN	hm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element;
2812	15926	29038	6.87	6.0E-46	AI884381.1	EST_HUMAN	hm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12 MER19 repetitive element;
6257	19431	32778	11.57	6.0E-46	AI635448.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Ku8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE;
7366	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	xa2d04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:U08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7541	20614	34091	0.67	8.0E-46	BF509740.1	EST_HUMAN	UIH-B14-agg-b-08-Q.U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	h01478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 6'
209	13492		5.31	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3617	16781	29796	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3617	16781	29797	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6874	20028	33438	1.52	5.0E-46	BF590442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:4156670 5'
7080	20174	33596	3.69	5.0E-46	BF347229.1	EST_HUMAN	Q75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7244	20372	33772	0.75	5.0E-46	AW582283.1	EST_HUMAN	QV4-S10212-120100-075-009 ST0212 Homo sapiens cDNA
7544	20616	34093	0.69	5.0E-46	BE549744.1	EST_HUMAN	7b38b05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	nc64609.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1740	14889	27981	2.89	4.0E-46	AW770544.1	EST_HUMAN	h188c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27982	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1
2798	15913	28021	7.4	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN) contains element MER37 repetitive element;
5563	18750	31786	2.1	4.0E-46	M38862.1	NT	Human endogenous retrovirus RTVL-P12
5553	18750	31787	2.1	4.0E-46	M38862.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12851	25565	31989	1.36	4.0E-46	AB002059.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
2369	15490	28620	0.94	3.0E-46	7657203	NT	Homo sapiens DNA for Human P2XM, complete cds
4513	17652	30840	1.21	3.0E-46	4508378	NT	Homo sapiens acidic 82 kDa protein mRNA (HSL15552), mRNA
4898	18028	31015	1.11	3.0E-46	273690.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4898	18028	31016	1.11	3.0E-46	273690.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
8949	22028	35569	12.45	3.0E-46	A1831462.1	EST_HUMAN	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
9206	22284	35824	0.61	3.0E-46	L08860.1	NT	THR repetitive element;
9206	22284	35825	0.61	3.0E-46	L08860.1	NT	Human AD amyloid mRNA, complete cds
11873	24861	38558	1.78	3.0E-46	D31765.1	NT	Human AD amyloid mRNA, complete cds
860	14037	27099	12.65	2.0E-46	AA468646.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1593	14748		3.78	2.0E-46	AA878246.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1671	14823	27905	5.63	2.0E-46	U76027.1	NT	Human mRNA for KIAA0061 gene, partial cds
5089	18217	31188	1.26	2.0E-46	AA399286.1	EST_HUMAN	repetitive element;
7653	20721	34197	7.1	2.0E-46	8910569	NT	repetitive element;
8280	21342		1.29	2.0E-46	BE869161.1	EST_HUMAN	z22/a11 s1 Scores_fetal_liver_spleen_INFLS_31 Homo sapiens cDNA clone IMAGE:431998 3'
11524	24960		1.82	2.0E-46	7657233	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12394	26040		1.4	2.0E-46	BF028864.1	EST_HUMAN	z59a02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE
12555	25031		1.57	2.0E-46	HA5391.1	EST_HUMAN	Q01730 RSP-1 PROTEIN.
12596	25401		3.31	2.0E-46	AA001786.1	EST_HUMAN	Mus musculus sperm tail associated protein (Sap), mRNA
12934	25923	31864	4.26	2.0E-46	AW27721.4.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
1281	14418	27483	4.31	1.0E-46	4502894	NT	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987326 5'
2356	15487	28619	4.89	1.0E-46	AW978516.1	EST_HUMAN	y322d01.r1 Scores_fetal_liver_spleen_INFLS_Homo sapiens cDNA clone IMAGE:206977 5'
							z184f12.r1 Scores_fetal_liver_spleen_INFLS_31 Homo sapiens cDNA clone IMAGE:428016 5'
							xq78h03.x1 NCI CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756769 3'
							Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
							EST390625 MAGE resequences, MAGE Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST483096 WATM1 Homo sapiens cDNA clone 483096
3321	16494	29511	2.12	1.0E-46	AA631912.1	EST_HUMAN	np78502.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens
4996	18124		3.13	1.0E-46	AB023197.1	NT	MT-11 mRNA. (HUMAN);
5817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6098	25818	32609	5.34	1.0E-46	8923762	NT	762801.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	25818	32610	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19902	33295	0.64	1.0E-46	BF196247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7n48607.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3687862 3' similar to contains element
11410	24471	38136	1.81	1.0E-46	AJ245621.1	NT	MER22 repetitive element;
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	762801.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens CTL2 gene
13176	25764		1.99	1.0E-46	AV715377.1	EST_HUMAN	602072284F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4215398 5'
787	13966		3.7	9.0E-47	AJ271735.1	NT	602072284F1 NCL CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4215398 5'
5047	18176	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
6506	19672	33039	0.86	9.0E-47	11425439	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11388	24449	38110	1.4	9.0E-47	11432209	NT	h93604.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006534 3' similar to TR:O75703 O75703
12874	26027	31675	1.84	9.0E-47	11417966	NT	h93604.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006534 3' similar to TR:O75703 O75703
1861	14907	28100	32.2	8.0E-47	Y18536.1	NT	HYPOTHETICAL 12.4 KD PROTEIN ;
1851	14997	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
2781	15897	29007	1.5	8.0E-47	5463855	NT	Homo sapiens similar to aldol-keto reductase family 1, member B1 (aldose reductase) (H. sapiens)
3089	16265	29283	2.04	8.0E-47	AJ229043.1	NT	(LOC63093), mRNA
3715	18978	29881	0.77	8.0E-47	AB041928.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3715	18978	29882	0.77	8.0E-47	AB041928.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
12962	25922		1.99	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens HLA-C gene, exon 5, individual 19323
2613	15737	28651	3.04	6.0E-47	AL163246.2	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9476	22533	36097	6.83	6.0E-47	AI695189.1	EST_HUMAN	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	AV683284 GSK Homo sapiens cDNA clone GKCASH11 5'
							Homo sapiens chromosome 21 segment HS21C046
							HSU77054 Human Homo sapiens cDNA clone N7
							hs28h02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286659 3'
							Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
							Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	10865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens GDC37 (cell division cycle 37, S. cerevisiae, homolog) (GDC37), mRNA
11036	24114		6.58	5.0E-47	M78590.1	EST_HUMAN	EST00739 Fetal brain, Striatum (cat#33208) Homo sapiens cDNA clone HFBCF07
1432	14585	27660	7.03	4.0E-47	4557566	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
6971	20199	33625	0.62	4.0E-47	BE938896.1	EST_HUMAN	MIR4-TN0108-280800-201-004 TN0108 Homo sapiens cDNA
8877	21767	35282	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822437 5'
8677	21767	35293	2.22	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822437 5'
8816	21897	35436	0.83	4.0E-47	AW983777.1	EST_HUMAN	RC3-BN0034-220300-015-05 BN0034 Homo sapiens cDNA
11936	24922		1.98	4.0E-47	AW515509.1	EST_HUMAN	xx66607.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	Q64262 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
558	13751	26779	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	14019	27075	3.99	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
968	14141	27202	10.04	3.0E-47	AL163284.2	NT	y54604.s1 Soares, multiple, cellular, 2Nbl-MSP Homo sapiens cDNA clone IMAGE:277327 3'
3376	16348	28582	0.97	3.0E-47	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4073	17228		6.01	3.0E-47	U63181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SDF1), mRNA, partial cds
4482	17822	30603	1.14	3.0E-47	M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19315	32654	4.68	3.0E-47	AW408800.1	EST_HUMAN	UIH-F-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6136	19315	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UIH-F-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6594	19852		1.71	3.0E-47	A122413.1	EST_HUMAN	q104407.x1 Soares, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7540	20813	34089	0.88	3.0E-47	A1816766.1	EST_HUMAN	w11108.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
7540	20813	34090	0.88	3.0E-47	A1819755.1	EST_HUMAN	w11108.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35654	0.77	3.0E-47	AW983796.1	EST_HUMAN	EST375969 MAGI resequences, MAGI Homo sapiens cDNA
9033	22112	35655	0.77	3.0E-47	AW983796.1	EST_HUMAN	EST375968 MAGI resequences, MAGI Homo sapiens cDNA
152	13377	26409	1.21	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
990	14162	27221	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
990	14162	27222	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1598	14751		0.95	2.0E-47	A1969276.1	EST_HUMAN	wq98602.x1 NCI CGAP_GCS Homo sapiens cDNA clone IMAGE:2479851 3'
1623	14776	27859	1.61	2.0E-47	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1712	14863	27852	4.49	2.0E-47	AA524514.1	EST_HUMAN	hg43h12.x1 NCI CGAP_C63 Homo sapiens cDNA clone IMAGE:837607 3'
4487	17007	30585	1.61	2.0E-47	4504866	NT	Homo sapiens finger protein (C3HC4 type) 8 (RNF8), mRNA
4503	17643	30628	1.87	2.0E-47	AA569592.1	EST_HUMAN	n23g07.s1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:914552
4503	17643	30629	1.67	2.0E-47	AA569592.1	EST_HUMAN	n23g07.s1 NCI CGAP_Prl Homo sapiens cDNA clone IMAGE:914552
4628	17764	30746	2.14	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA
4833	18063	31046	1.25	2.0E-47	AW985168.1	EST_HUMAN	EST377239 MAGI resequences, MAGI Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18366		0.71	2.0E-47	AI041126.1	EST_HUMAN	ov61h03.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5804	19083	32407	0.9	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signalling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE779476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7878	25854		1.34	2.0E-47	LO9731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34754	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8915	21894	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9690	22739	36308	1.27	2.0E-47	11526138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	26073	31653	3.96	2.0E-47	R42423.1	EST_HUMAN	y02e08.x1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:29866 3' similar to contains OFR
12394	26076		1.87	2.0E-47	AL163209.2	NT	repetitive element ;
1437	14590	27663	5.42	1.0E-47	AI333429.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3926	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	q99h03.x1 Soares fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1631189 3'
3926	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5187	18309	31275	2.4	1.0E-47	AW813908.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
7199	20054	33464	10.76	1.0E-47	AI880886.1	EST_HUMAN	RC3-ST0197-130400-017-P02 ST0197 Homo sapiens cDNA
9099	22148		4.24	1.0E-47	AW664948.1	EST_HUMAN	at19606.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355589 3' similar to gb:M22995
10584	23599	37205	2.26	1.0E-47	L30115.1	NT	RAS-RELATED PROTEIN RAP-1A (HUMAN);
1643	14795	27879	3.84	9.0E-48	AF223391.1	NT	h84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978672 3' similar to gb:M26326
3846	16809	29823	0.73	9.0E-48	BF359647.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
5797	18987	32290	1.1	9.0E-48	BE888109.1	EST_HUMAN	Poplo hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5797	18987	32291	1.1	9.0E-48	BE888109.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6226	19401	32751	0.57	9.0E-48	AI833188.1	EST_HUMAN	CM2-MT0100-310700-290-105 MT0100 Homo sapiens cDNA
6355	18625	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
11376	24439	36088	3.06	9.0E-48	BE393813.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
1279	14436		1.75	8.0E-48	4501900	NT	at75h09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
1280	14436		1.65	8.0E-48	4501900	NT	OB0844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN ;
							AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000678 5'
							601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							h661b03.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3205	16380	29390	5.72	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW768477.1	EST_HUMAN	h061b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
4041	17197	30208	0.66	8.0E-48	4504118	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13398		2.58	7.0E-48	AB033035.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13398		18.69	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	14880	27761	1.98	7.0E-48	6912719	NT	Homo sapiens tousel-like kinase 1 (TLK1), mRNA
1667	14819	27902	5.39	7.0E-48	6730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6885	19843	33233	24.01	7.0E-48	11418831	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
12125	25105	38809	2.98	7.0E-48	R19623.1	EST_HUMAN	y937502.1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE:34747 5'
3687	16950	29858	0.88	6.0E-48	A176111.1	EST_HUMAN	w69h03.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6183	19359	32707	0.84	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-75, complete cds
6924	20239	33674	0.93	6.0E-48	11420995	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7828	25849	34173	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9323	22399	35953	1.57	6.0E-48	AF028816.1	NT	Homo sapiens putative oncogene p/cdcin mRNA, partial cds
9741	22806	36382	1.87	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
8890	22930	36514	2.84	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.a1 Stralagene HNT neuron (#937293) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
3384	18465	28560	1.48	5.0E-48	4828801	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
8774	21853	35395	1.04	5.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
2828	15943	29053	1.02	4.0E-48	R43715.1	EST_HUMAN	Ha140 f Adult heart, Clontech Homo sapiens cDNA clone a140-f
11200	24269	37905	3.11	4.0E-48	AB20420.1	EST_HUMAN	h047402.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
12050	25031	38737	1.75	4.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
1416	14570	27643	1.91	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
2032	15173	28282	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2032	16173	28283	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3505	16872	29682	0.93	3.0E-48	AF172453.1	NT	Homo sapiens opid growth factor receptor mRNA, complete cds
3721	16982	29888	0.9	3.0E-48	AW664531.1	EST_HUMAN	h114b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
4382	17605		0.63	3.0E-48	AA009541.1	EST_HUMAN	P59555 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
6015	19189	32316	2.08	3.0E-48	BE084571.1	EST_HUMAN	Z04q03.r1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'
7189	20282	33735	1.07	3.0E-48	AF087913.1	NT	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
8585	21666		3.73	3.0E-48	AA659830.1	EST_HUMAN	Human endogenous retrovirus HERV-P-147D
							nv0305.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element;